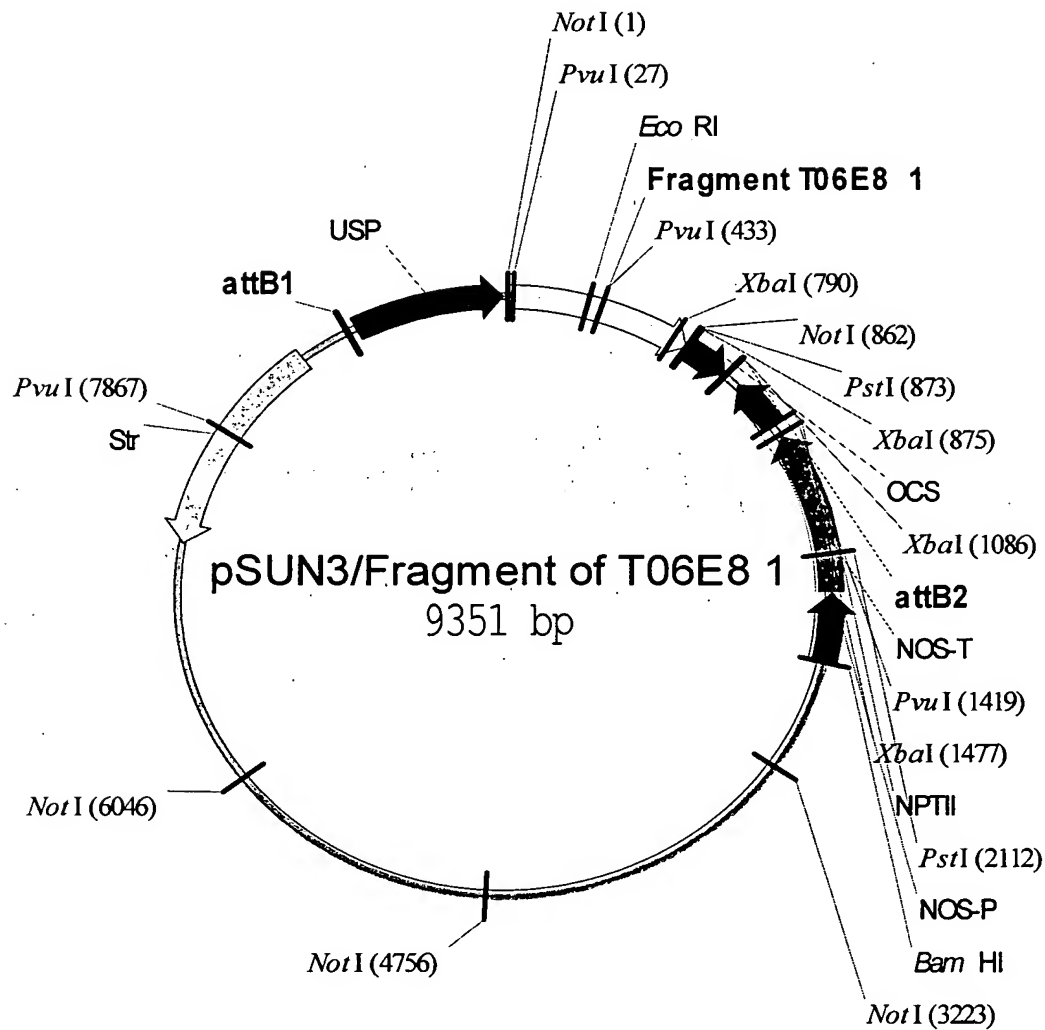


Figure 1: Vector map of pSUN3CeLPLAT



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Figure 2: Amino acid sequence alignment of *C. elegans* LPLATs (Ce-T06E8.1 and Ce-F59F4.4) with the *M. musculus* LPAAT (Mm-NP061350).

```

1                                     50
Mm-NP061350 MELWPGAWTA LLLLLELLLS TLWFCSSSAK YEFKMAFYNG WELFLAILAI
Ce-T06E8.1  ...MENFWSI VVFLELSIF ILYNISTVCH YMYRISEYF TILLHGMEVC
Ce-F59F4.4  .....MTF LAILEFVIAVL LLLAQLPVIG FYIRAVYEGM CLLIGGFLGG

51                                     100
Mm-NP061350 PVC AVRGRNV ENMKIERLL LHAKYLYGER VEVGAHHFP PTQPYVWVSN
Ce-T06E8.1  VTMIPSWLNG KGADYMFHSF FYWCKWTGVH TTVYGYEKTQ VEGPAVATCN
Ce-F59F4.4  LASIPFGKSP NNHFRMFKIF QAMTWPMGVR FELRNSEILH DKKPYITLHAN

101                                    150
Mm-NP061350 HQSSLDLGLM MEVLPRDCVP IAKRELLWAG SAGLACWLAG TTEIDRKRRTG
Ce-T06E8.1  HQSSLDLGLM ASIWPKNQCV MMKRILAVVP FFNLGAYFSN TTEIDRYNRE
Ce-F59F4.4  HQSALDVLGM SFAWPVDCV MLKSSLKMLP GFNLCAVLC D SVYINRFSKE

151                                    200
Mm-NP061350 DATSVMSIVA QTILTDQVRV WVFPEGTRNH NGSMTPFKRG AFHILAVQAQV
Ce-T06E8.1  RAMASVDYCA SEMKNRNLKL WVFPEGTRNR EGGFTPEKKG AFNIAVRAQI
Ce-F59F4.4  KALKTVDTTL HEIVTKKRKV WLYPEGTRNA EPELLPEKKG AFILAKQAKI

201                                    250
Mm-NP061350 PIIPIVMSSY QDFYSKKERR FTSPGRCQVR VLPPVSTEGL TPDDVPALAD
Ce-T06E8.1  PIIPVVFSDY RDFYSKPGRY FKNDGEVVIR VLDAIPKGL TLDDVSELS D
Ce-F59F4.4  PIVPCVFSSH KFFYSHAEKR LTS.GNCILD ILPEVDSS.. KFD SIDDLSA

251                                    285
Mm-NP061350 SVRHSMLTIF RETSTDGLGG GDCLKKPGGA GEARL
Ce-T06E8.1  MCRDVMLAAY KEVTLEAQQR NATRRGETKD GKKSE
Ce-F59F4.4  HCRKIMQAGR EKIDAEAAANL NI.....

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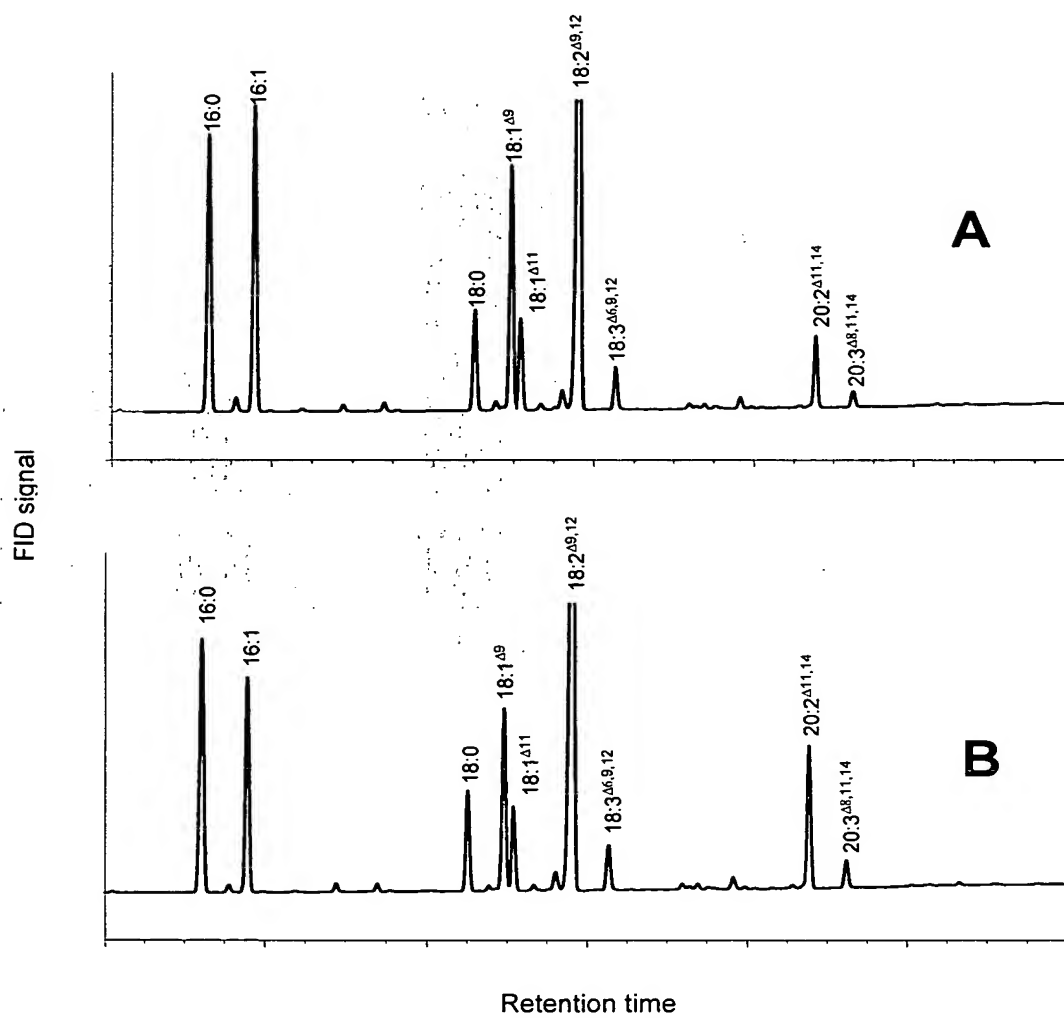
Figure 3: Fatty acid profiles of transgenic C13ABYS86 *S. cerevisiae* cells

Figure 4: Elongation of exogenously applied  $18:2^{\Delta 9,12}$  and  $18:3^{\Delta 9,12,15}$ , respectively, following their endogenous  $\Delta$ -6-desaturation (data from figs 2 and 3).

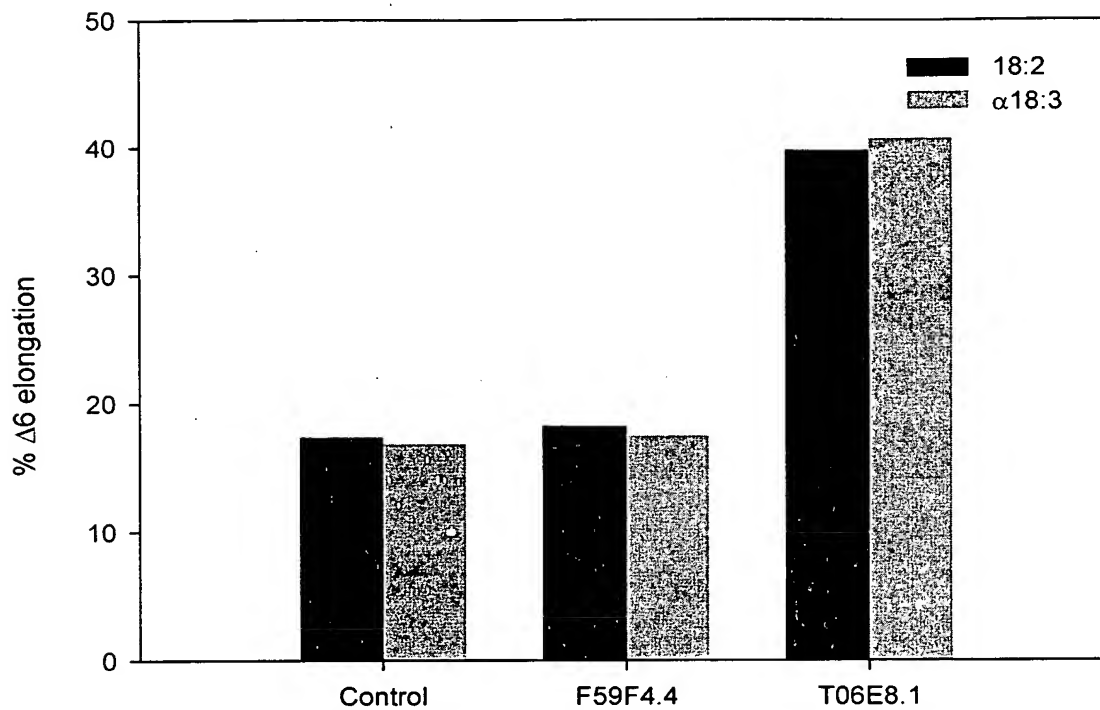


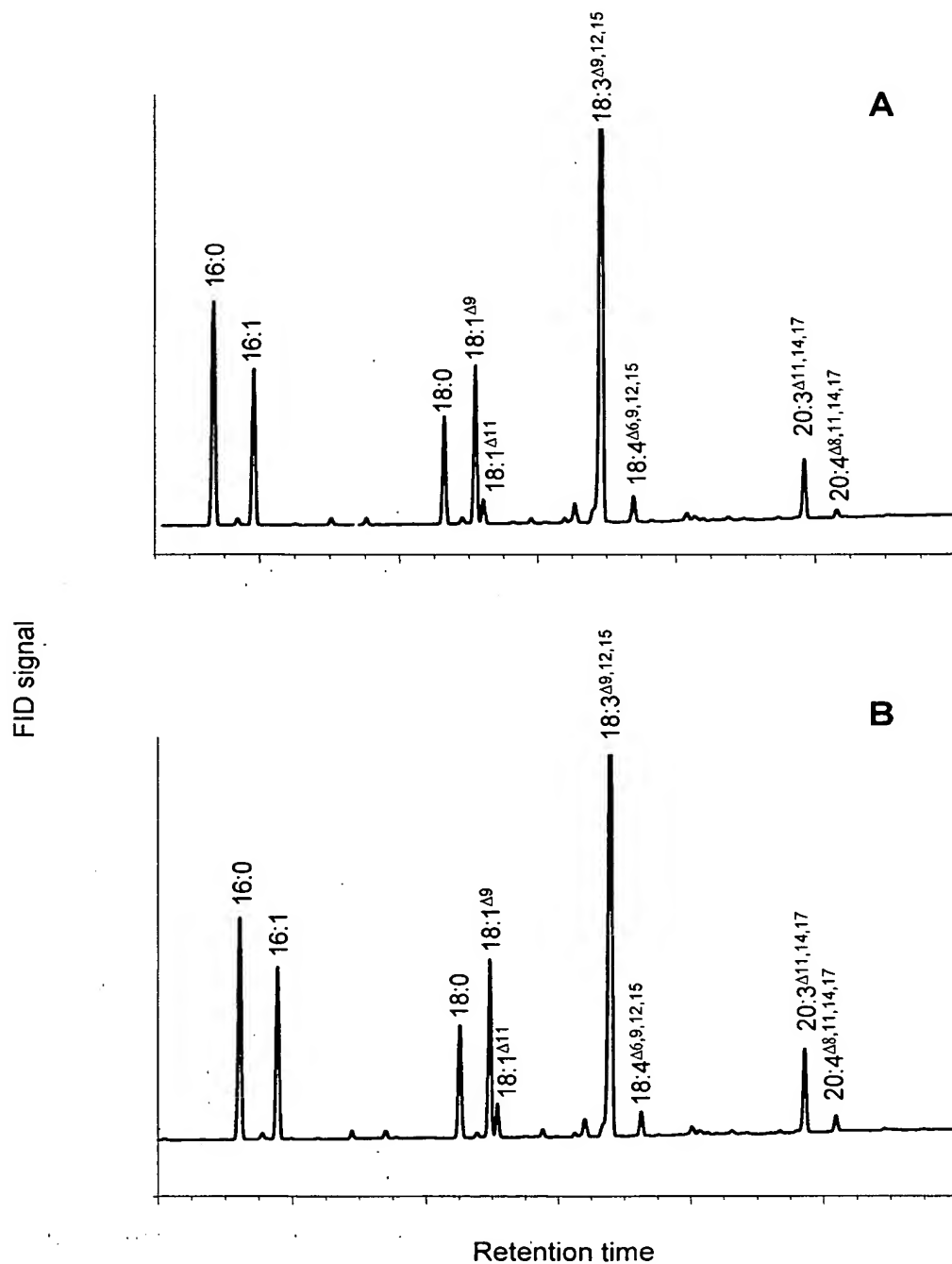
Figure 5: Fatty acid profiles of transgenic C13ABYS86 *S. cerevisiae* cells

Figure 6: Acyl-CoA composition of transgenic INVSc1 yeasts which had been transformed with the vectors pESCLeu PpD6Pse1/pYes2 (A) or pESCLeu-PpD6-Pse1/pYes2-T06E8.1 (B).

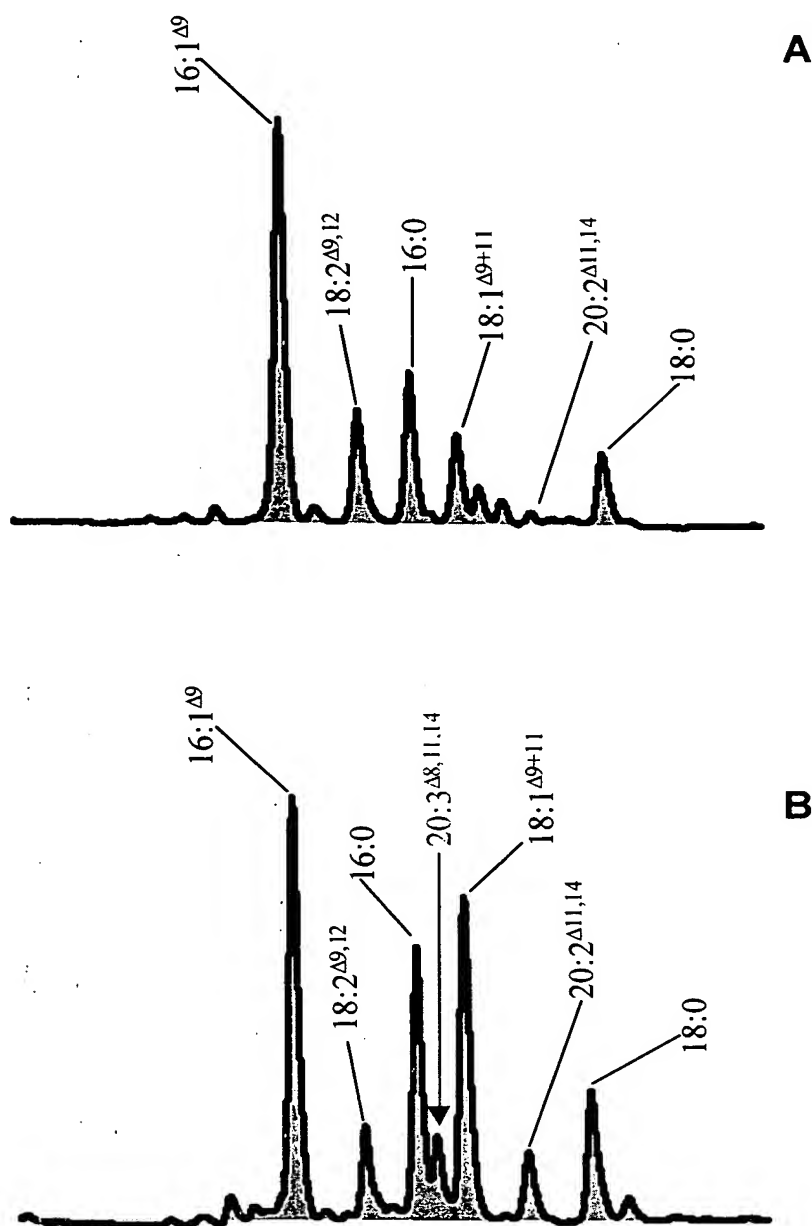


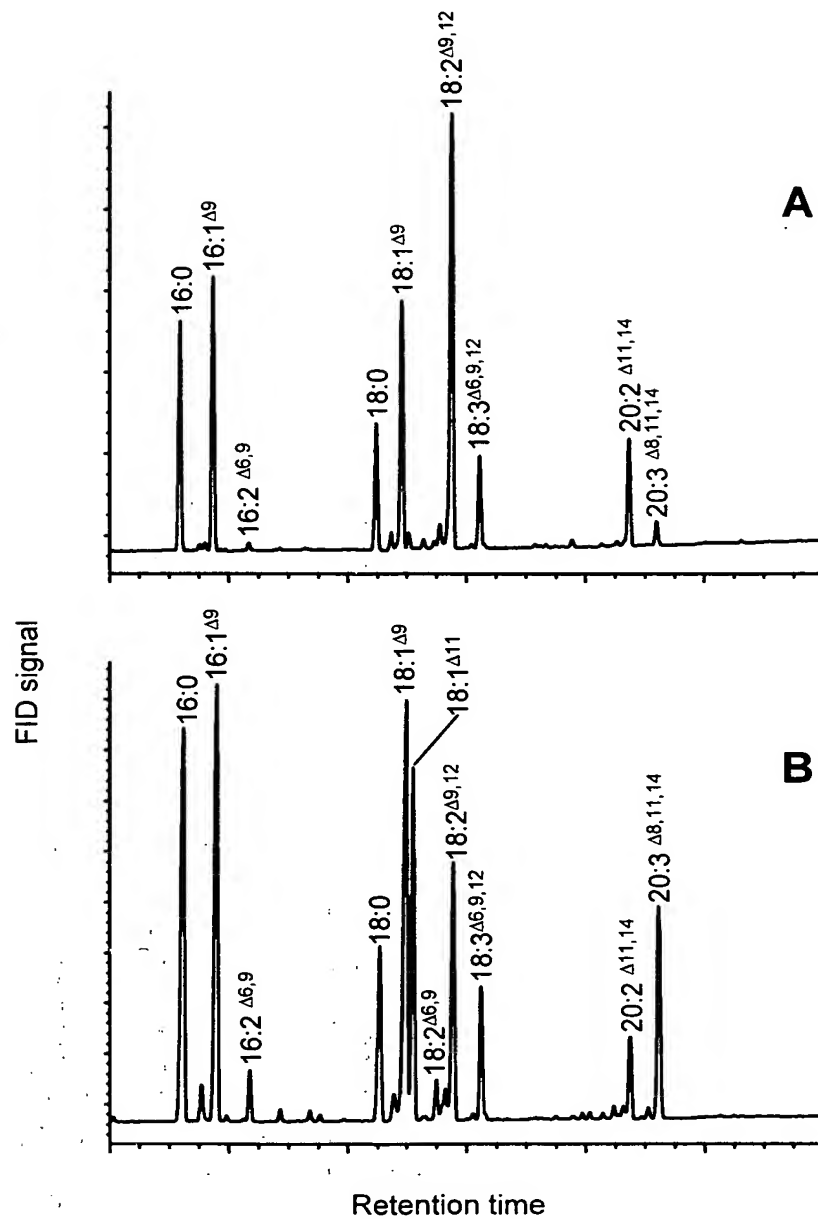
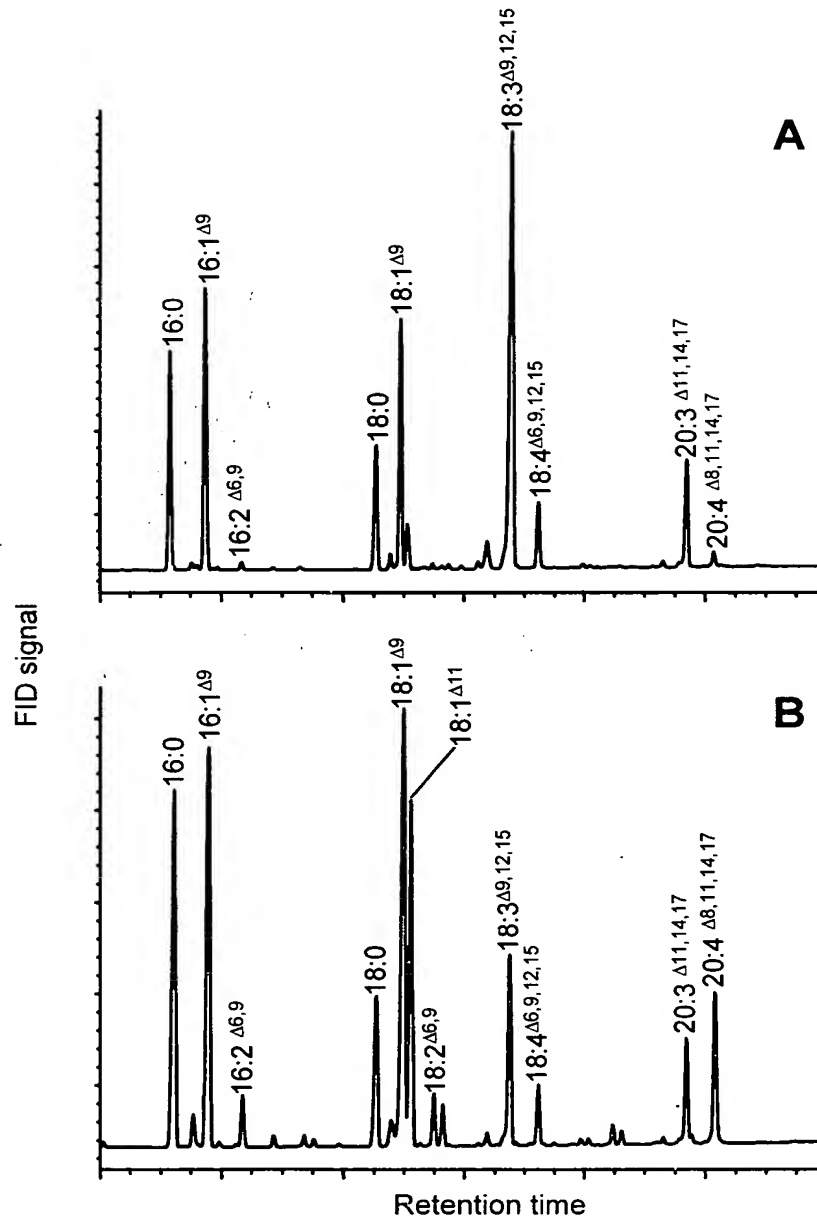
Figure 7: Fatty acid profiles of transgenic INVSc1 *S. cerevisiae* cells

Figure 8: Fatty acid profiles of transgenic INVSc1 *S. cerevisiae* cells.



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Figure 9A: Vector map of pGPTV LeB4-700 + T06E8.1

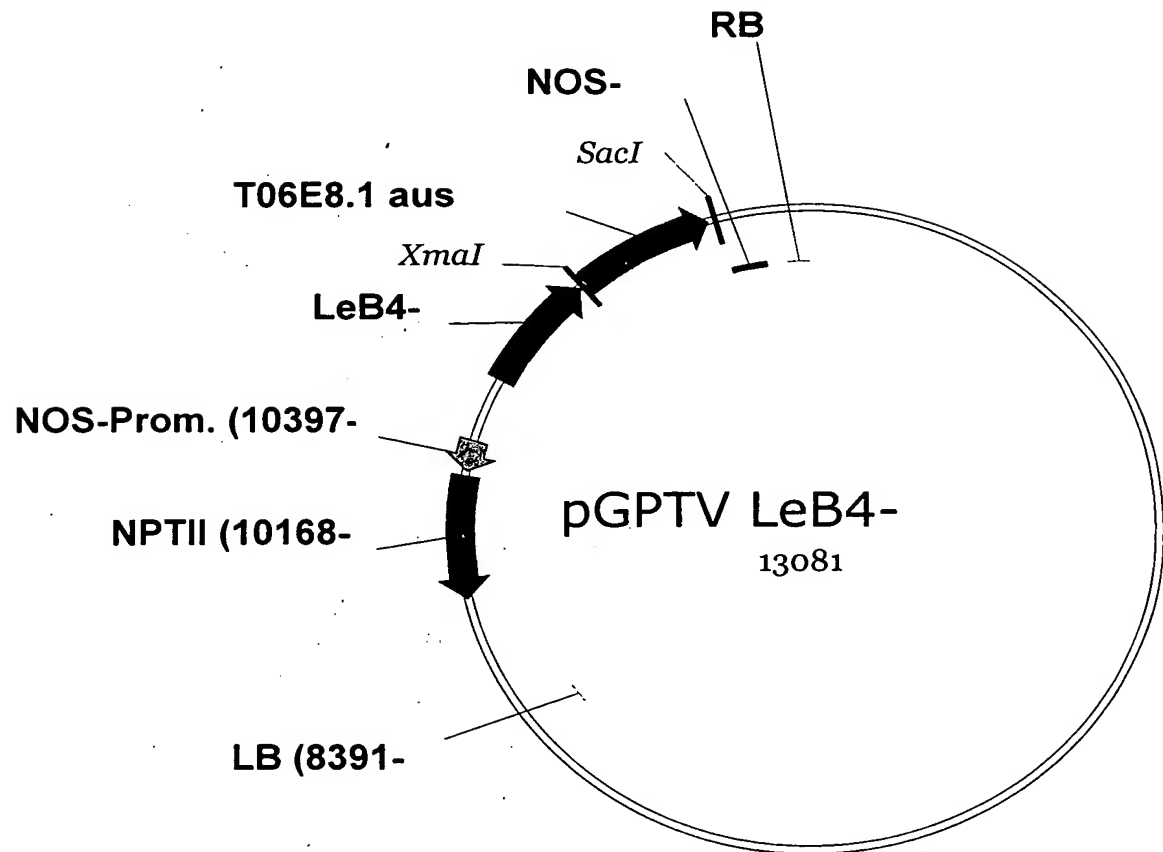
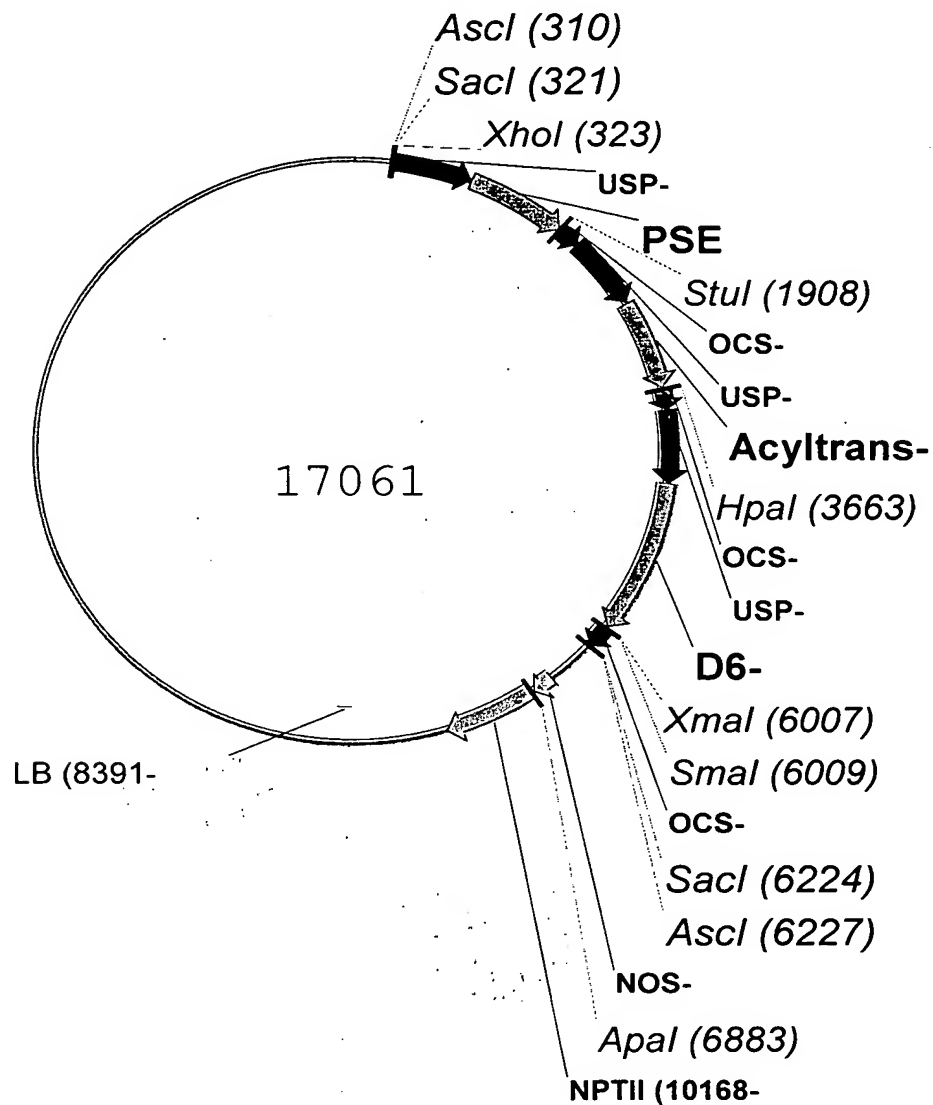


Figure 9B: Vector map of pGPTV USP/OCS-1,2,3 PSE1(Pp)+D6-Des(Pt)+2AT (T06E8-1)

pGPTV/USP/OCS-1,2,3 PSE1(Pp) D6-Des(Pt)-2 AT(T06E8-1)



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Figure 10A: Biosynthetic pathway of LCPUFAs

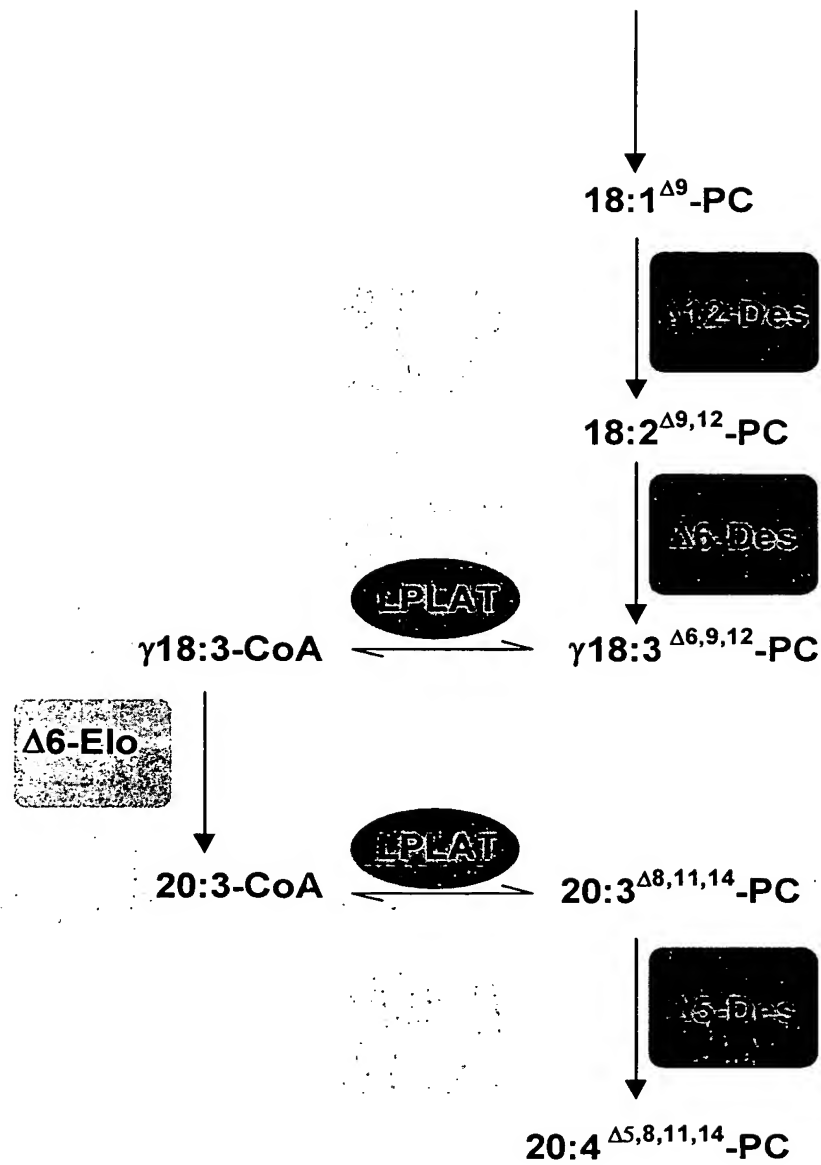


Figure 10B: Biosynthetic pathway of LCPUFAs

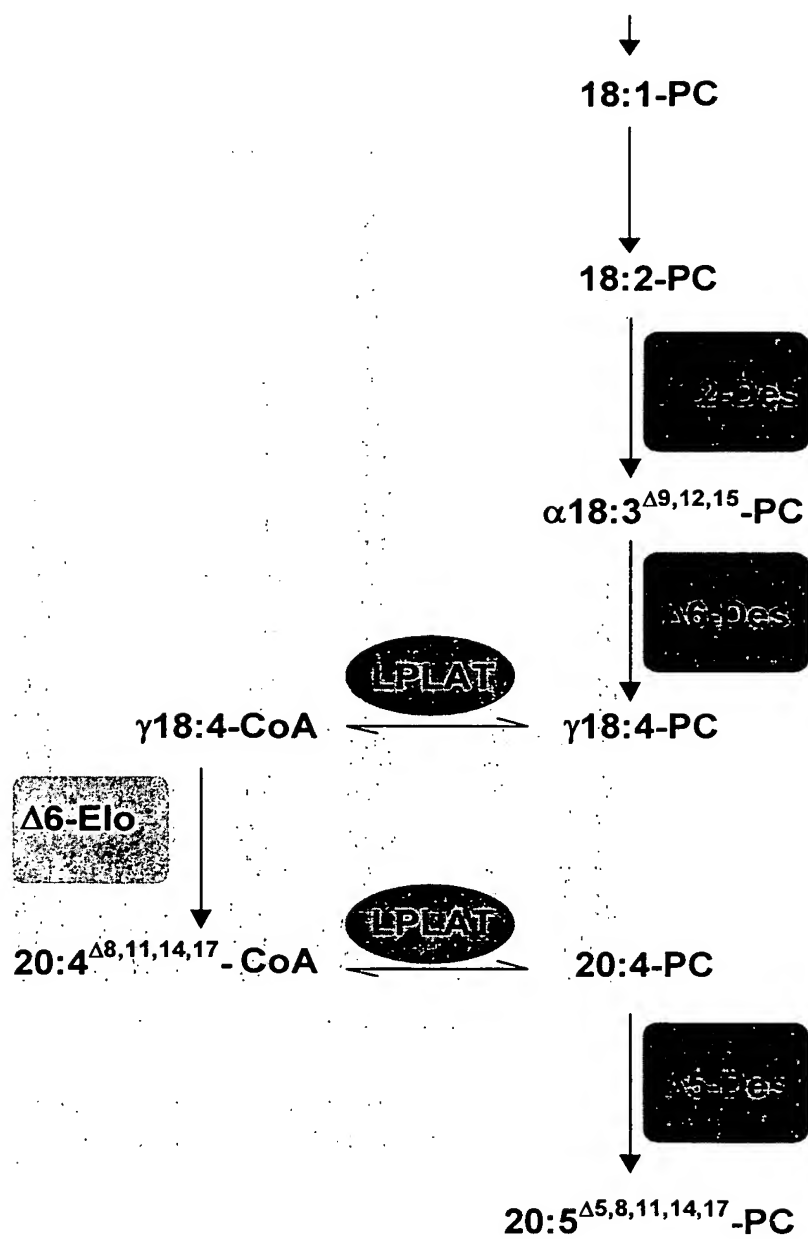
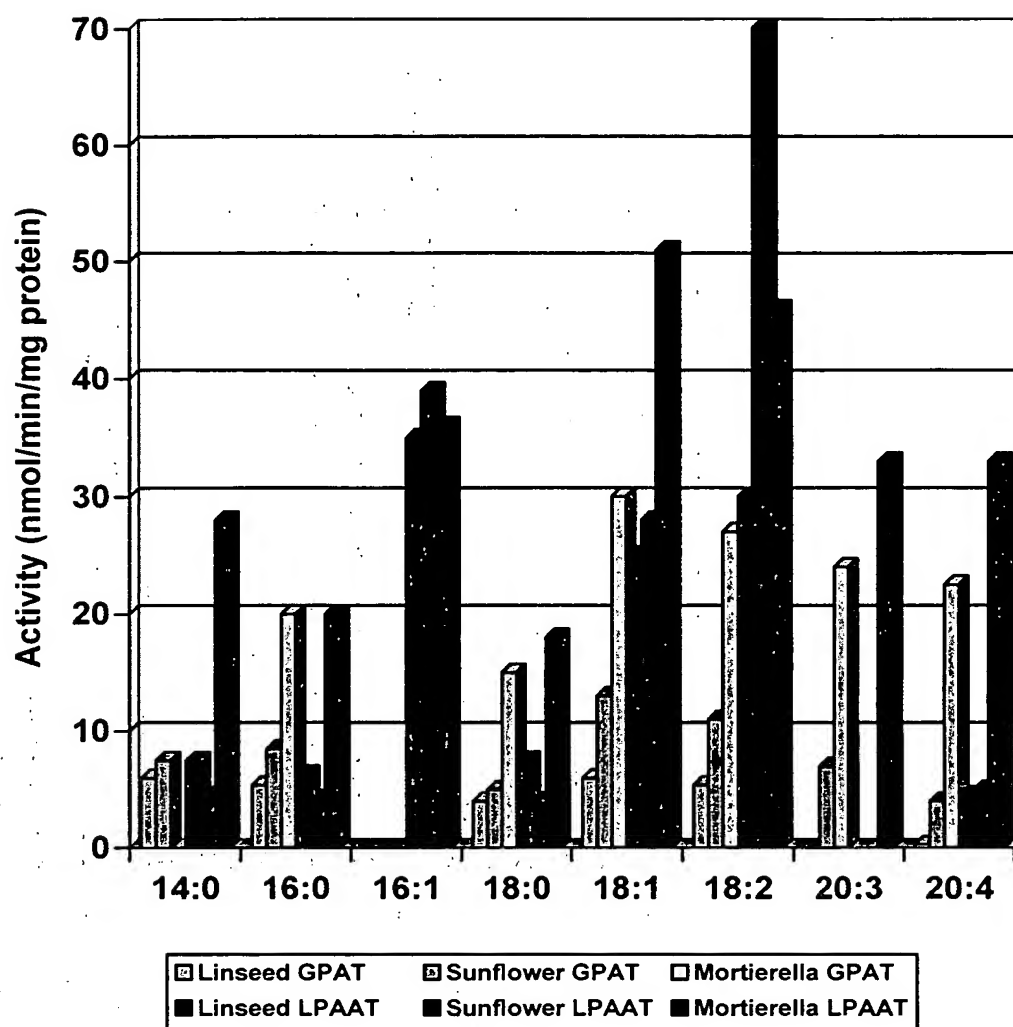
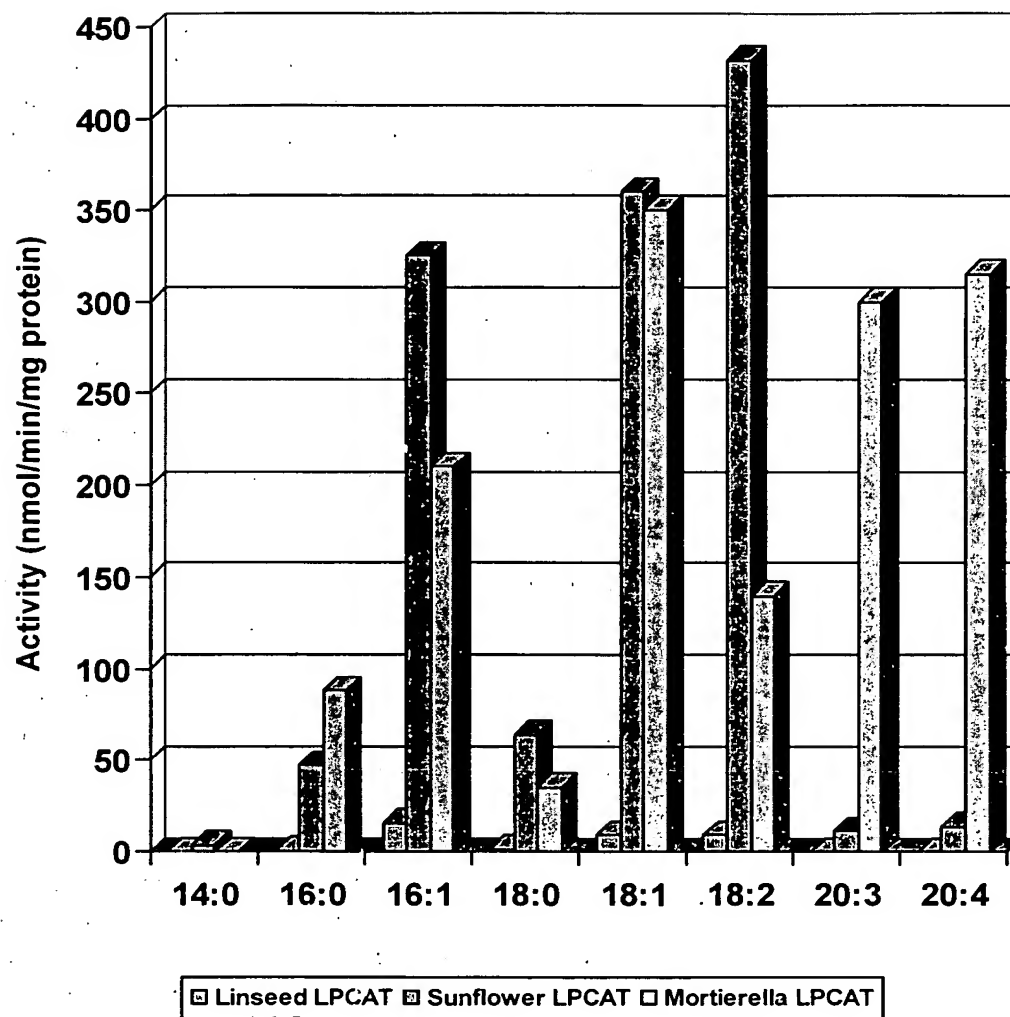


Figure 11: Comparison of GPAT and LPAAT substrate specificities in linseed, sunflower and *Mortierella alpina*



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Figure 12: Comparison of LPCAT substrate specificity in linseed, sunflower and -  
*Mortierella alpina*



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Figure 13: Alignment of SEQ ID NO: 2 with Swiss Prot database

	1	50
Q9JZ47	.....MSSNKASFFTRL	
Q9JU41	.....MSSNKASFFTRL	
Q59601	.....MSSNKASFFTRL	
Q9HW50	.....MARLRLLLRSARL	
SEQ ID NO: 2	.....MSAWTRAKTAVGL	
O35259	METIMDDEVTKRTSAEELESWNLLSRTNYNFQYISLRLTILWGLGVLI	RY
	51	100
Q9JZ47	RRLCRLAVWLFKTGKNLRGIDGG.CPESRNRAVIELGRGVLAALD.....	
Q9JU41	RRLCRLTVWLFKTGKNLRGIDGG.CPESRNRAVIELGRGVLAALD.....	
Q59601	RRLCRLTVWLFKTGKNLRGIDGG.CPKSRNRAVIALGKGALAALD.....	
Q9HW50	LGLVALGLGLAAWVSLRERLPGADVTPLRQRLTRWWLARLCAALP.....	
SEQ ID NO: 2	LTLAPARIVFLVTVLGTYGLTVAACRLGVPKSFVLGLTRCVARLTLWGL	
O35259	CFLPLRIALAFTGIGLLVVGTTMVGYPNGRFKEFLSKHVHLMCYRICV	
	101	150
Q9JZ47	..IGLEVGRPAPEHPNG..VLVAANHVSULDIFAMS.AVYPSSFIAKQEI	
Q9JU41	..IGLEVGRPAPEHPNG..VLVAANHVSULDIFAMS.AVYPSSFIAKQEI	
Q59601	..IGLEVGRPAPEHPNG..VLVAANHVSULDIFAMS.AVYPSSFIAKQEI	
Q9HW50	..FEVRVSGEAPRQP...MLWVANHVSWTDIPLLG.ALAPLTFLSKAEV	
SEQ ID NO: 2	GFYHIEVSCDAQGLREWP.RVIVANHVSYLEILYFMSTVHCPSFVMKKTC	
O35259	RALTAIITYHNRKNRPRNGGICVANHTSRIDVIFASDGYAMVGQVHGG	
	151	200
Q9JZ47	KSWPVLGKMGQNAGTVFINRNSRR.....DIEPINRAVCETLQRGQ	
Q9JU41	KSWPVLGKMGQNAGTVFINRNSRR.....DIEPINRAVCETLQRGQ	
Q59601	KSWPVLGKMGQNAGTVFINRNSRR.....DIEPINRAVCETLQRGQ	
Q9HW50	RAWPLAGWLAEKAGTLFIRRGSG.....DSRLINQRLAEQLHRGR	
SEQ ID NO: 2	LRVPLVGYIAMELGGVIVDREGGQSASAIIRDRVQEPDRDSSEKHHAQ	
O35259	LMGVIQRAMVKACPHVWFERSEVK.....DRHLVAKRLTEHVQDKS	
	201	250
Q9JZ47	..NVSFFPEARTSSGLGLLPFKAALFQSAIDAGAKVLAVALRYYDETGKR	
Q9JU41	..NVSFFPEARTSSGLGLLPFKAALFQSAIDAGAKVLAVALRYYDETGKR	
Q59601	..NVSFFPEARTSSGLGLLPFKAALFQSAIDAGAKVLAVALRYYDETGKR	
Q9HW50	..NLLIFPEGTTTNGESLRTFHGRMASALEAGVAVQPVAISYRRDGVDP	
SEQ ID NO: 2	..PLLVFPEGTTTNGESCLLQFKTGAFR...PG.APVLPVVLEFPIDKARG	
O35259	KLPILIFPEGTCINNTSVMMFKKGSFEIG....ATVYPVAIKY..DPQFG	

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	251	300
Q9JZ47	TARPSYADVGLPTCLWRIVSMKKLTIRVDFVCVADAAE.....	
Q9JU41	TARPSYADVGLPTCLWRIVSMKKLTIKVDFVCVADAAE.....	
Q59601	TARPSYADVGLPTCLWRIVSMKKLTIKVDFVCVADAAE.....	
Q9HW50	AQAPFIGDDDLLSHLGRLLRGERGSVHIQLLEPIPSQ.....	
SEQ ID NO: 2	DFSPAYESVHTPAHLLRMLAQWRHRLRVRYLPLYEPSAAEKVDADLYARN	
O35259	DAFWNSSKYGMVTYLLRMMTSWAIVCSVWYLPMTRE.....	

	301	349
Q9JZ47	...SEDRYALKDKIEESIRAVVADDADIIV.....	
Q9JU41	...SEDRYALKDKIEESIRAVVADDADIIV.....	
Q59601	...SEDRYALKDKIEESIRAVVADDADIIV.....	
Q9HW50	...GLDRAELARQAQQAVRLALFGTAAPTQTRRAA.....	
SEQ ID NO: 2	VRDEMARALKVPTVEQSYRDKLVYHADLMPHYQKAGPGALYLYVRPDL	
O35259	.....KDEDAVQFANRVKSAIARQEDW.....	



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Figure 14: Alignment of SEQ ID NO: 5 with Swiss Prot database

	1	50
Q9C9P8	MEVCGDLKSDNLKNRPLTPLRILRGLMILLVFLSTAFMFLLYFAPIAALG	
Q9SFJ1	MEVCGDLKSDNLKNRPLTPLRILRGLMILLVFLSTAFMFLLYFAPIAALG	
Q9LHN4	.....MEKKSVPNSDKLSLIRVLRGIICLMVLVSTAFMMLIFWGFLSAVV	
SEQ ID NO: 5	.....	
Q9SDN3	.....	
Q9XFW4	.....MAMAAVIVPLGILFFISGLVVNLLQAVCYVLV	
	51	100
Q9C9P8	LRLLSVQQSRKVVSLLIFGLWLALWPYLFETVNGTTVVFSGDIIP...VEK	
Q9SFJ1	LRLLSVQQSRKVVSLLIFGLWLALWPYLFETVNGTTVVFSGDIIP...VEK	
Q9LHN4	LRLFSIRYSRKCVSFFFGSWLALWPFLFEKINKTKVIFSGDKVP...CED	
SEQ ID NO: 5	.....MDVVKVIFAGDKVP...KEN	
Q9SDN3	.....MGKE	
Q9XFW4	RPMSKNTYRKINRVVAETLWLELVWIVDWWAGVKIQVFADDETFRNMKE	
	101	150
Q9C9P8	RVLLIANHRTEVDWMYLWNIALRKGCGLGYIKYVLKSSLMKLPFIGWGPHV	
Q9SFJ1	RVLLIANHRTEVDWMYLWNIALRKGCGLGYIKYVLKSSLMKLPFIGWGPHV	
Q9LHN4	RVLLIANHRTEVDWMYFWDLALRKQIGNIKYVLKSSLMKLPFIGWAFHL	
SEQ ID NO: 5	RVMVMCNHRTEVDWMIWNLAIRKKGKIGYCKYAVKNSVKNLPLFGWAFYV	
Q9SDN3	HALVISNHRSDIDWLVGWVLAQRSGCLGSSLAVMKKSSKFLPVIGWSMWF	
Q9XFW4	HALVVCNHRSDIDWLVGWILAQRSGCLGSALAVMKKSSKFLPVIGWSMWF	
	151	200
Q9C9P8	LEFIPVERKREVDEPVLLQMLSSFKDPQEPLWLALFPEGTDFTTECKKRS	
Q9SFJ1	LEFIPVERKREVDEPVLLQMLSSFKDPQEPLWLALFPEGTDFTTECKKRS	
Q9LHN4	FEFIPVERRWEVDEANLRQIVSSFKDPRDALWLALFPEGTDYTEACKQRS	
SEQ ID NO: 5	FEFLMLHRKWEVDAPVIKTYIDSFQDKRDPLWLVVFPPEGTDFTSEAKRDTG	
Q9SDN3	SEYLFLEERSWAKDEGTLKSGVQRLKDFPQPFWLALFVEGTRFTQAKLLAA	
Q9XFW4	SEYLFLEERNWAKDESTLQSGLQRLNDFPRPFWLALFVEGTRFTEAKLKAA	
	201	250
Q9C9P8	QKFAAEVGLPALSNVLLPKTRGFGVCLEVLHNSLDAVYDLTIAYKPRCP.	
Q9SFJ1	QKFAAEVGLPALSNVLLPKTRGFGVCLEVLHNSLDAVYDLTIAYKPRCP.	
Q9LHN4	KKFAAENGLPILNNVLLPRTKGFSCLQELSCSLDAVYDVTIGYKTRCP.	
SEQ ID NO: 5	NAIGREKGYPELVNVLQPRTRGFVTCLSQSRCSLDAVYDLTIIGYKKRCP.	
Q9SDN3	QEYAAATGLPVPRNVLIPTKGFVTVAVSQMRSFAPAIYDVTVAIPKSSPA	
Q9XFW4	QEYAASELVPVPRNVLIPTKGFVSAVSNMRSFVPAIYDMTVAIPKTSPP	

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	251	300
Q9C9P8	SFMDNVFGTDPSEVHIHVRRVLLKEIPANEAESSAWLMDSFKLKDKLLSD	
Q9SFJ1	SFMDNVFGTDPSEVHIHVRRVLLKEIPANEAESSAWLMDSFKLKDKLLSD	
Q9LHN4	SFLDNVYGI EPSEVHIHRRINLTQIPNQEKDINAWLMNTFQLKDQLLND	
SEQ ID NO: 5	LFINNFGTDPSEVHIHRRIPISEIPQSEDCMTQWLYDLFYQKQMLAS	
Q9SDN3	PTMLRRLFEGRPSVVHVHIKRHVMDLPETDEAVAQWCKDIFVAKDALLDK	
Q9XFW4	PTMLRRLFQGPSVVHVHIKCHSMKDLPEPEDEIAQWCRDQFVAKDALLDK	

	301	350
Q9C9P8	FNAQKGFPNQRPEEELSVLKCIATFAGKQQQVTKPSCQKVFLLLNQSSDE	
Q9SFJ1	FNAQKGFPNQRPEEELSVLKCIATFAGKQQQVTKPSCQKVFLLLNQSSDE	
Q9LHN4	FYSNGHFPNEGTEKEFNKKYLINCLAVIAFTTICTHLTFFSSMIWFRIY	
SEQ ID NO: 5	FSKTGSFPDSGIE.ESPLNIVEGVCNVALHVVLSGWVFWCLFHSVWLKLY	
Q9SDN3	HTVEQTFGDQQLKVTGRPLKSLLVVTAWACLLILGALKFLYWSSLLSSWK	
Q9XFW4	HIAADTFPGQKEQNIGRPIKSLAVVSWACLLTLGAMKFLHWSNLFSSWK	

	351	400
Q9C9P8	KESKKAVAQHPFTDTLDHLFQVEHSISCFLYMHYINLSTCHLISLYE...	
Q9SFJ1	KESKKAVAQHPFTDTLDHLFQVEHSISCFLYMHYINLSTCHLISLYE...	
Q9LHN4	VSLACVYLTSATHFNLRSVPLVETAKNSLKLVNK.....	
SEQ ID NO: 5	VAFASLLAFSTYFDWRPKPVYSSLRTRKIV.....	
Q9SDN3	GIAFSALGLGVVTVLMQILIRFSQSERSTPAPVAPTNNKNKGESSGKPEK	
Q9XFW4	GIALSAFGLGIITLCMQILIRSSQSERSTPAKVAPAKPKDNHQSGPSSQT	

	401
Q9C9P8	.....
Q9SFJ1	.....
Q9LHN4	.....
SEQ ID NO: 5	.....
Q9SDN3	QQ.....
Q9XFW4	EVEEKQK

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Figure 15: Alignment of SEQ ID NO: 35 with Swiss Prot database

	1	50
P04180	.....	MGP
Q08758	.....	MGP
Q9MZ04	.....	MGL
Q9DDJ6	.....	MGR
Q9Y2B3	.....	MGL
SEQ ID NO: 35	MCSISCGSTPQQLCHYRKSGELITRKSRAAIRWWRYGQQCKVLLPLDLIR	
	51	100
P04180	PGSPWQWVTLLGLLLPP.....	AAPFWLLNVLFPPHTTPK
Q08758	PGSPWQWVPLLLGLLLPP.....	AAPFWLLNVLFPPHTTPK
Q9MZ04	PGSPWQWVLLLLLELLLP.....	AAPFWLLNVLFPPHTTPK
Q9DDJ6	TGAGFALLTLLLLLPQP.....	ASQFWLFNVLFPPSTPE
Q9Y2B3	HLRPYRVGLLPLGLLFL.....	LLLMLLADPALP.....
SEQ ID NO: 35	SSSQFFIVVLTTLTFLFTTCGAVHTAAQDRSFATLSQRSRASLFSVGRAQ	
	101	150
P04180	AELSNHTRPVILVPGCLGNQLEAKLDKPDVVN.WMCYRKTEDEFFTIWLDL	
Q08758	AELSNHTRPVILVPGCLGNQLEAKLDKPDVVN.WMCYRKTEDEFFTIWLDL	
Q9MZ04	AELSNHTRPVILVPGCLGNQLEAKLDKPDVVN.WMCYRKTEDEFFTIWLDL	
Q9DDJ6	APPTNSTPPVVLVPGCLGNQLEAKLDKPDVVN.WMCYRKTEDEFFTIWLDL	
Q9Y2B3	...AGRHPVVLVPGDLGNQLEAKLDKPTVVH.YLCSKKTESYFTIWLNL	
SEQ ID NO: 35	ARNKHHLAPVIVPGTGGNQLAARLTADYEANKPWCYSFRKDYFRLWLDV	
	151	200
P04180	NMFLPLGVDCWIDNTRVVYNRSSGLVSNAPGVQIRVPGFGKTYSV EYLDL	
Q08758	NMFLPLGVDCWIDNTRVVYNRSSGLVSNAPGVQIRVPGFGKTYSV EYLDL	
Q9MZ04	NMFLPLGVDCWIDNTRVTYNHSSGRVSNAPGVQIRVPGFGKTYSV EYLDL	
Q9DDJ6	NTFLPVGWDCWIDNTRVVYNRTSRKMSNAPGVHVRVPGFGKTYSV EYLDQ	
Q9Y2B3	ELLLPVIIIDCWIDNIRLVYNKTSRATQFPDGVDRVPGFGKTFSL EFLDP	
SEQ ID NO: 35	KTLFPPFTTCFADRLSLDYNPQSDAYSNIKGVKTRVPFFGTTEGMEYLDP	
	201	250
P04180	SK..LAGYLHTLVQNLVNNGYVRDET VRAAPYDWRLEPGQOE.....EYY	
Q08758	SK..LAGYLHTLVQNLVNNGYVRDET VRAAPYDWRLEPGQOE.....EYY	
Q9MZ04	SK..LAGYMHTLVQNLVNNGYVRDET VRAAPYDWRLGPKQOE.....EYY	
Q9DDJ6	SK..LAGYLHTLVQNLVNNGYVRDQTVRAAPYDWRVGPQE QP.....EYF	
Q9Y2B3	SKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENG.....PYF	
SEQ ID NO: 35	SLKFLTGYMIHLVNALKAHGYENGKSLYGAPYDFRFAPGPHASNVALEYL	

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	251	300
P04180	RKLAGLVEEMHAAYG.KPVFLIGHSLGCLHLLYFLLRQPQAWKDRFIDGF	
Q08758	HKLAGLVEEMHAAYG.KPVFLIGHSLGCLHLLYFLLRQPQAWKDRFIDGF	
Q9MZ04	RDLARLVEEMHATYG.KPVFLIGHSLGCLHLLHFLHQPQSWKDRFIDGF	
Q9DDJ6	QNLKALIEEMHDEYQ.QRVFLIAHSMGNLNVLYFLLQQRQAWKDQYIGGF	
Q9Y2B3	LALREMIEEMYQLYG.GPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAF	
SEQ ID NO: 35	KDLKDLIETAYSVNANEPVVILAHSMGGLWTLFFLNQQSMEWRNKYVSRF	
	301	350
P04180	ISLGAPWGGSIKPMLVLASGDNQGIPIIMSSIKLKEEQRITTTSPWMFPSPR	
Q08758	ISLGAPWGGSIKPMLVLASGDNQGIPIIMSSIKLKEEQRITTTSPWMFPSPR	
Q9MZ04	ISLGAPWGGSIKPMQVLASGDNQGIPIIMSSIKLKEEQRITTTSPWMFPSS	
Q9DDJ6	ISLGAPWGGSVKPLRVLASGDNQGIPLMSNIKLREEQRMTTTSPWMFPTS	
Q9Y2B3	VSLGAPWGGVAKTLRVLASGDNNRIPVIGPLKIREQQRSVSTSWLLPYN	
SEQ ID NO: 35	VSVATPWGGAVEQMMTFASGNPEGVFPVNSLVVREEQRRSESNLWLLPVR	
	351	400
P04180	MAWPEDHVFISTFSFNYTGRDFQRRFADLHFEEGWYMWLQ.SRDLLAGLP	
Q08758	LAWPEDHVFISTFSFNYTGRDFQRRFADLHFEEGWYMWLQ.SRDLLAGLP	
Q9MZ04	EVWPEDHVFISTFSFNYTIRDYQRRFVDVHFEEGWYMWLQ.SRDLLAGLP	
Q9DDJ6	LAWPEDHIFISTPSYNYTYRDKQFFTDVNLEDGWYMWED.MKDLLKGLP	
Q9Y2B3	YTWSPEKVFVQTPPTINYTLRDYRKFQDIGFEDGWLMRQD.TEGLVEATM	
SEQ ID NO: 35	RCFR.DRPLVITSSRNYTAGDMEQFLCDIGFPEGVAPYKSRIPLTDILQ	
	401	450
P04180	APGVEVYCLYGVLPTPRTYIYDHGFPYTDVPVGLYEDGDDTVATRST.E	
Q08758	APGVEVYCLYGVLPTPRTYIYDHGFPYTDVPDVLYEDGDDTVATRST.E	
Q9MZ04	APGVEVYCLYGVLPTPSTYIYDHDFPYTDPLDVLYEDGDNTVATRSME	
Q9DDJ6	PPGVDTYCLYGTGYPTVETIYIDEHFPYEDPVDMIYGDGDDTVNRRSS.E	
Q9Y2B3	PPGVQLHCLYGTGVPTPDSFYYES.FPDRDPK.ICFGDGDGTVNLSA.L	
SEQ ID NO: 35	PPQVPVTLIHGYGVPTAETLSYEK.KGFDNHPEITEGDGDGTVNVCSLTA	
	451	500
P04180	LCGLWQGRQPQPVHLLPLHGIQHLNMVFSNLTLEHINAILLGAYRQGPPA	
Q08758	LCGLWQGRQPQPVHLLPLRGIQHLNMVFSNQTLEHINAILLGAYRQGPPA	
Q9MZ04	LCSQWQGRQPQPVHLLPLHRIQHLNMVFSNQTLEHINDILLGAYRHGNPV	
Q9DDJ6	LCKRWRNQKQKVHIQELRGIDHLNMVFSNLTSSINEILLGSSQVGAGT	
Q9Y2B3	QCQAWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG.....	
SEQ ID NO: 35	VVEEWERVAGQELEMIALHGKQHMQILHDDHSVQVIVDAILNVTPQEQLM	
	501	524
P04180	SPTASPEPPPPPE.....	
Q08758	SLTASPEPPPPPE.....	
Q9MZ04	PPAASPRPLTPE.....	
Q9DDJ6	KEHGELGQMGALKSSLEAGRGRGN	
Q9Y2B3	.....	
SEQ ID NO: 35	FH.....	

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Figure 16: Alignment of SEQ ID NO: 23 with Swiss Prot database

	1	50
P10349	.....	
Q9FEP9	.....MFILSSSSSTLPSAPPFSSSTTSIFLSFSRVSLPPSSSSSLK...	
Q39639	MFILSAVSSSSSSSSSVPSLPPFSLSPSISLSFSRVSLPPSSSSSSSL	
Q9FEQ0	.....MFILSSSSSLPSPLSLSSSRVSLPPPSSSSSLN..	
Q9M4V1	.....MLVPSALPRVSRVSAAARFSVSGVGSSPALSSRS	
SEQ ID NO: 23	.....MPSLFRAKRNGRRTPGNAVTN...	
	51	100
P10349	.....MAELIQDKESAQSAATAAAAS	
Q9FEP9	..LLPLSLQFGPPKLAS.SCSLRFSASRAMAELIQDKESAQSAATAAAAS	
Q39639	KLFLPLSLHFTPPKLSSPHSFLRFSASRAMAELIQDKESAHTPSTTDVTR	
Q9FEQ0	..LLPLSPHFQPPNLAC...SCSVASRSTAELLHDFKHSHTAASADEAR	
Q9M4V1	CTSLDSSVRSSLRRCPCGIYTSRTKAVVEAVESKASAREWRSVAVKRAVLA	
SEQ ID NO: 23	.....FGKSEFH.....R..EIS...GSTRATTQVAEATTAGLRE	
	101	150
P10349	SGYERRNEPAHSRKFLDVRSEEELLSCIKKETEAGKLPPNVAAGMEELYQ	
Q9FEP9	SGYERRNEPAHSRKFLDVRSEEELLSCIKKETEAGKLPPNVAAGMEELYQ	
Q39639	N.....DPPHSRAFLDLRSEEELLSCIRRETEAGKLPSNVAAGMEELYQ	
Q9FEQ0	N.....HLPHSRAFLDVRSEQELLSYIRREAEAGKLPSNVAAGMEELYQ	
Q9M4V1	SDTGAEEEVGHSRSFLRARSEEELLSYIRKEVETGRLSSDIANGLEELYY	
SEQ ID NO: 23	TIEDRAIDGHSHSFEGIQSEEELMQVIEKEVESGRLPKRAGAGMVELYR	
	151	200
P10349	NYRNAVIESGNPKADEIVLSNMTVALDRILLDVEDPFVFSHHKAIREFP	
Q9FEP9	NYRNAVIESGNPKADEIVLSNMTVALDRILLDVEDPFVFSHHKAIREFP	
Q39639	NYKNAVFESGNPKADEIVLSNMTVALDRILLDVEDPFMFSPHHKAIREFP	
Q9FEQ0	NYKNAVLKSGNPKADEIVLSNMTVALDRILLDVEEPFVFSPHHKAVREFP	
Q9M4V1	NYRNAVLQSGDPRANKIILSNMAVAFDRILLDVEDPFTFSPHHQAIREFP	
SEQ ID NO: 23	NYRDAVVSSGVENAMDIVVKVMSTVLDRILLQFEEPFTFGSHHKRMVEPY	
	201	250
P10349	DYYIFGQNYIRPLIDFGNSFVGNLFLFKDIEEKLQQGHNVVLISNHQTEA	
Q9FEP9	DYYIFGQNYIRPLIDFGNSFVGNLFLFKDIEEKLQQGHNVVLISNHQTEA	
Q39639	DYYTFGQNYVRPLIDFGNSFVGNLFLFKDIEEKLHQQGHNVVLISNHQTEA	
Q9FEQ0	DYYTFGQNYVRPLIDFGNSFVGNPFLFKDIEEKLHQQGHNVVLISNHQTEA	
Q9M4V1	DYYMFGQNYIRPLIDFRRSYIGNISIFSDMEEKLQQGHNIVLMSNHQTEA	
SEQ ID NO: 23	DYYTFGQNYVRPLLDFRNSYLGNLKIFDQIEKNLKEGHNVIFLSNHQTEA	

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	251	300
P10349	DPAIISLLEKTNPYIAENTIFVAGDRVLADPLCKPFSIGRNLCVYSKK	
Q9FEP9	DPAIISLLEKTNPYIAENTIFVAGDRVLADPLCKPFSIGRNLCVYSKK	
Q39639	DPAIISLLEKTNPYIAENMIYVAGDRVIADPLCKPFSIGRNLCVYSKK	
Q9FEQ0	DPAIISLLEKTSPIYAENMIYVAGDRVIVDPLCKPFSIGRNLCVYSKK	
Q9M4V1	DPAIALLERTNSHIAETMVVAGDRVLTDPCKPFSMGRNLLCVYSKK	
SEQ ID NO: 23	DPAVMALLLEHSHPYLAENLTYVAGDRVLDPFCKPFSMGRNLLCVYSKK	

	301	350
P10349	HMFDIPELTETKRKANTRSLKEMALLRGGSQLIWIAPSGGRDRPDPSTG	
Q9FEP9	HMFDIPELTETKRKANTRSLKEMALLRGGSQLIWIAPSGGRDRPDPSTG	
Q39639	HMLDIPELAETKRKANTRSLKEMALLRGGSQLIWIAPSGGRDRPDPSTG	
Q9FEQ0	HMFDIPELAETKRKANTRSLKEMALLRGGSQLIWIAPSGGRDRPDPSSG	
Q9M4V1	HMDDVPELIEMKRRANTRSLKEMALLRGGSQLIWIAPSGGRDRPDPSTG	
SEQ ID NO: 23	HIHDVPDLAEMKIKANAKTLRQMTILLRQGGQYGG.....	

	351	400
P10349	EWYPAPFDASSVDNMRRLIQHSDVPGHLFPLALLCHDIMPPPSQVEIEIG	
Q9FEP9	EWYPAPFDASSVDNMRRLIQHSDVPGHLFPLALLCHDIMPPPSQVEIEIG	
Q39639	EWYPAPFDASSVDNMRRLLQHSGAPGHLYPLALLCYDIMPPPSQVEIEIG	
Q9FEQ0	EWLPAPFDASSMDNMRRLIQHSGVPGHLCPLALLCYDIMPPPSQVEIEIG	
Q9M4V1	EWHPAPFDVSSVDNMRRLEHSSVPGHIYPLSLLCYEVMPPPPQVEKQIG	
SEQ ID NO: 23	.....	

	401	450
P10349	EKRVIAFNGAGLSVAPEISFEEIAATHKNPEEVREAYSKALFDSVAMQYN	
Q9FEP9	EKRVIAFNGAGLSVAPEISFEEIAATHKNPEEVREAYSKALFDSVAMQYN	
Q39639	EKRVISFNGTGLSVGPEISFDEIAASRDNPDEVREAYSKALYDSVAKQYN	
Q9FEQ0	EKRVISFNGVGLSLAPAISFEAIAATHRNPDEAREAYSKALFDSVSMQYN	
Q9M4V1	ERRTISFHGVGLSVAPELNFNELTAGCETPEEAKEAFSQALYNSVGEQYN	
SEQ ID NO: 23	.....	

	451	476
P10349	VLKTAISGKQGLGASTADVLSQPW.	
Q9FEP9	VLKTAISGKQGLGASTADVLSQPW.	
Q39639	VLKAAIDGKQELEASVADVLSQPWI	
Q9FEQ0	VLKAAIYGRQALRASTADVLSQPWI	
Q9M4V1	VLKSAIHEHRGLNASNSIISLSQPWQ	
SEQ ID NO: 23	.....	

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Figure 17: Alignment of SEQ ID NO: 27 with Swiss Prot database

	1	50
SEQ ID NO: 27	MEGGGSIIALPLGLMFLFSGFFINILQLLSVLFILPFSRRAYRVVNMIMM	
Q9XFW4	.MAMAAVIVPLGILFFISGLVVNLLQAVCYVLRPMSKNTYRKINRVVA	
Q40119	MAIPAAAFIVPISLLFFMSGLVVNFIQAVFYVLRPISKDTYRRINTLVA	
Q9SDN3	.....	
Q41745	MAIPLVLVVLPLGLLFLLSGLIVNAIQAVLFVTIRPFSKSFYRRINRFLA	
Q9SYC8	MKIPAAALVFIPVGVLFLLISGLIVNIIQLVFFIIVRPFSRSLYRRINKNVA	
	51	100
SEQ ID NO: 27	EVLWSELIWLLDWWANVKVKVYTPKESWEHLGKEHALLICNHRSDIDWL	
Q9XFW4	ETLWLELVWIVDWWAGVKIQVFADDETFNRMGKEHALVVCNHRSDIDWL	
Q40119	ELLWLELVWVIDWWAGVKVQLYTDTESFRLMGKEHALLICNHRSDIDWLI	
Q9SDN3	.....MGKEHALVISNHRSDIDWL	
Q41745	ELLWLQLVWVVDWWAGVKVQLHADEETYRSMGKEHALIISNHRSDIDWLI	
Q9SYC8	ELLWLQLIWLFDDWWACIKINLYVDAETLELIGKEHALVLSNHRSDIDWLI	
	101	150
SEQ ID NO: 27	GWIIAQRLGCLGGTRAVMKKSTKFLPVIGWSMWFSEYVFLSRDWAKDEKV	
Q9XFW4	GWILAQRSGCLGSALAVMKKSSKFLPVIGWSMWFSEYLFERNWAKDEST	
Q40119	GWVLAQRCGCLSSSIAMVKKSSKFLPVIGWSMWFSEYLFERNWAKDENT	
Q9SDN3	GWVLAQRSGCLGSSLAVMKKSSKFLPVIGWSMWFSEYLFERSWAKDEGT	
Q41745	GWILAQRSGCLGSTLAVMKKSSKFLPVIGWSMWFSEYLFERSWAKDEKT	
Q9SYC8	GWVMAQRVGCLGSSLAIMKKEAKYLPPIGWWSMWFSDYIFLERSWAKDENT	
	151	200
SEQ ID NO: 27	LKNGYSSLKGFPRTLWVALFVEGTRFTKAKLEAAQKFAADTGLRVPRHVL	
Q9XFW4	LQSQLQRLNDFPRPFWLALFVEGTRFTEAKLAAQEYAASSELVPRNV	
Q40119	LKSQLQRLNDFPKPFWLALFVEGTRFTKAKLLAAQEYAASAGLPVPRNV	
Q9SDN3	LKSGVQRLKDFPQPFWLALFVEGTRFTQAKLLAAQEYAAATGLPVPRNV	
Q41745	LKWGLQRLKDFPRPFWLALFVEGTRFTPAKLLAAQEYAASQGLPAPRNV	
Q9SYC8	LKAGFKRLEDFPMTFWLALFVEGTRFTQEKLEAAQEYASIRSLPSPRNV	
	201	250
SEQ ID NO: 27	VPRTKGFVSAVENLREFVPVYDMTVAISKELPNPTMIRIFRGQPSVVHV	
Q9XFW4	IPRTKGFVSAVSNMRSFVPAIYDMTVAIPKTSPPPTMLRFLKGQPSVVHV	
Q40119	IPRTKGFVSAVSNMRSFVPAIYDLTVAIPKTTEQPTMLRFLRGKSSVVHV	
Q9SDN3	IPRTKGFVTAVSQMRSFAPAIYDVTVAIPKSSPAPTMLRFLFEGRPSVVHV	
Q41745	IPRTKGFVSAVSIMRDFVPAIYDTTVIVPKDSPQPTMLRILKGQSSVIHV	
Q9SYC8	IPRTKGFVSAVSEIRSFVPAIYDCTLTVHNNQPTPTLLRMFSGQSSEINL	

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	251	300
SEQ ID NO: 27	HVRRVPMSDLPEGANAISKWCHDAFHKDDRLEQHEKENTFGEDLYIPIE	
Q9XFW4	HIKCHSMKDLPEPEDEIAQWCRDQFVAKDALLDKHIAADTFPGQKEQNIG	
Q40119	HLKRHLMKDLPKTDDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVQDIG	
Q9SDN3	HIKRHVMRDLPETDEAVAQWCKDIFVAKDALLDKHTVEQTFGDQQLKVTG	
Q41745	RMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTFD.EEIRPIG	
Q9SYC8	QMRRHKMSELPETDDGIAQWCQDLFITKDAQLEKYFTKDVFSDELVHQIN	

	301	350
SEQ ID NO: 27	RPLKPLIIVISWAITLLAAAWFLRR..VLSTWKGIWVAGVLVVVMLCV	
Q9XFW4	RPIKSLAVVSWACLLTLGAMKFLHWSNLFSSWKGIASAFGLGIITLCM	
Q40119	RPMKSLVVVSWMCLLCLGLVKFLQWSALLSSWKGMITTFVLGIVTVLM	
Q9SDN3	RPLKSLLVVTAWACLLILGALKFLYWSSLLSSWKGIAFSALGLGVTVLM	
Q41745	RPVKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFTAAGMALVTGVM	
Q9SYC8	RPIKPLIVVIIWLGLVFGGFKLLQWLSIVASWKIILLFVFFLVIATITM	

	351	391
SEQ ID NO: 27	QILVMSSQSERSSDPAKKANQKQAASVAHLGKTD.....	
Q9XFW4	QILIRSSQSERSTPAKVAPAKPKDNHQSGPSSQTEVEEKQK	
Q40119	HILIRSSQSEHSTPAKTRARQTAENPK.....	
Q9SDN3	QILIRFSQSERSTPAPVAPTNNKNKGESSGKPEKQQ.....	
Q41745	HVFIMFSQAERSSSARAARNRVKKE.....	
Q9SYC8	QILIQSSESQRSTPAKRPLQEQLISA.....	



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Figure 18: Alignment of SEQ ID NO: 8 with Swiss Prot database

	1	50
SEQ ID NO: 8	MESTADVMSDDDPILLNGLETPLLAEFPLGERPTIGPEAPVNPFPHEPDG	
P42322	.....	
Q9NKW7	.....	
Q9XFJ4	.....MGQREDIRTLSNEYEVDIPRRGGLSVVRGTRRRRTLHSGQHHE	
O35259	.....	
Q9FF57	.....	
	51	100
SEQ ID NO: 8	GWKTNNNEWNYFQMMKSILLIPLLLVRLVSMITIVAFGYVWIRICLIGVTD	
P42322	.....	
Q9NKW7	.....	
Q9XFJ4	VVAIKTLR.RFGPPPAPEKKS LNKS RVPQAAL ISETLLTNELLVMIKIVE	
O35259	.....METIMDDEVTKRTSAEELESWNLLSRTNYN.	
Q9FF57	.....MIEQLGLIIIMGLIHYQSERVKPREWLKLSSSENSR	
	101	150
SEQ ID NO: 8	PLFKPFNPCRRLWGIRLVARAVMFTMGYYYIPIKGPAPHRSEAPIIVS	
P42322	.....	
Q9NKW7	.....	
Q9XFJ4	DVSPHPNVIHLYDVCEDPSGVHLILELCSGGELFDRIAGQARYNEEGAAA	
O35259	...FQYISLRLTILWGLGVLI RYCFLLPLRIALFTGIGLLVVGTTMVG Y	
Q9FF57	LG.NTKTNHRRSFTGDVSYEQRDLLDISPTLTEAAGAIVDFHCFKTCRCF	
	151	200
SEQ ID NO: 8	NHIGFLDPIFVFYRHLPAIVSAKENVEMPIIGLFLQALQIIPVDRDQAQS	
P42322	.....	
Q9NKW7	.....	
Q9XFJ4	VVRQIAKGLEALHGASIVHRDLKPENCLFLNKDENSPLKIMDFGLSSIED	
O35259	LPNGRFKEFLSKHVHLMCYR.....	
Q9FF57	TLAFGWIIIFLSLFIPVNALLK.....	
	201	250
SEQ ID NO: 8	RHHAAGNVRRRAVDNMWVSHVMLFPQGTTNGRAIIAFKTGAFSPGLPVQP	
P42322	.....	
Q9NKW7	.....	
Q9XFJ4	FANPVVGLFGSIDYVSPEALSREKITT KSDIWSLGVILYILLSGYPPFIA	
O35259	.....	
Q9FF57	.....GQDRLRKKIER	

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	251	300
SEQ ID NO: 8	MVIRYPHKYVNPSCWDQGGPLVVVLQLMTQFINHMEVEYLPVMKPTVREM	
P42322	.....	
Q9NKW7	.....	
Q9XFJ4	PSNRQKQQMILNGQFSFDEKWTWKNISSSAKQLISSLLKVDPNMRPTAQEI	
O35259	ICVR.ALTAIITYHN.....	
Q9FF57	VLVEMICSFFVASWTG.....	
	301	350
SEQ ID NO: 8	KYPHEFASRVRSEMAKALGIVCTEHSFLD...IKLALAAEKLKQPSGRSL	
P42322	.....MGTNTSSLRP	
Q9NKW7	.....MGN	
Q9XFJ4	LEHPWVTGDLAKQEQMDAEIVSRLQSFNARRKFRAAAMASILSSSFSLRT	
O35259	.....RKNRPRN.....GG	
Q9FF57	.....VVKYHGPRPSIRP...KQ	
	351	400
SEQ ID NO: 8	VEFARMEKLFRLDFPTAKEYLEKFSAMDRTHSGF..VTFEELCTALDLP.	
P42322	EEVEEMQKGTNFTQKEIKKLYKRFKKLDKDGNGT..ISKDEFLMIPELA.	
Q9NKW7	ENSLPMELC SNFDPDEIKRLGKRFRKLDLDNSGS..LSVDEFMTLPQL.	
Q9XFJ4	KKLKKLVGSYDLKPEELENLSHNFKKICKNGENSTLLEFEEVLKAMEMSS	
O35259	ICVANHTSRIDV IIFASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFE.	
Q9FF57	VYVANHTSMIDFIVLEQMTAFVIMQKHPGWVGLLQSTILESVCIWFN.	
	401	450
SEQ ID NO: 8	RSPITKQVFNLFDKDGHSINFRFLAGLAFVSSHTSFSSTMEAAFKACD	
P42322	VNPLVKRVISIFDENGDSVNFKEFIAALSVFNAQGDQQRKLEFAFKVYD	
Q9NKW7	QNPLVQRVIDIFD TDNGEVD FKEFIEGVSQFSVKGDKLSKLRFAFKIYD	
Q9XFJ4	LVPLAPRIFDLFDNNRDGTVDMRIIGGFSSSLKYSQGD.DALRLCFQVYD	
O35259	RSEVKDRHLVAKRLTEHVQDKSKLPILIFPEGTCINNT.SVMMFKKGSFE	
Q9FF57	RSEAKDREIVAKKLRDHVQGADSNPLLIFPEGTCVNNN.YTVMFKKGAFE	
	451	500
SEQ ID NO: 8	VNGDGTLSRDEVERSLLDIFPELPPI.....TVFKLFDTLINHDEKIS	
P42322	IDGDGYISNGELFTVLKMMVGNNLSD.VQLQQIVDKTILEADEDGDGKIS	
Q9NKW7	MDKDGYSNGELFQVLKMMVGNNLKD.TQLQQIVDKTIIHADADGDGKIS	
Q9XFJ4	TDRSGCISKEEVESMLRALPEDCLPINITEPGKLDEIFDLMDANS DGKVT	
O35259	IGATVYPVAIKYDPQGFDAFWNSSKYG.....MVTYLLRMMTSWAIVCSV	
Q9FF57	LDCTVCPIAIKYNKIFVDAFWNSRKQS.....FTMHLLQLMTSWAVVCEV	

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	501	550
SEQ ID NO: 8	WEEFSSFLQRNPEYLAIIIYAHPTLLKPPTSTS.....	
P42322	FEEFAKTLSHQDLENKMTIRL.....	
Q9NKW7	FEEFCAVVGNMMDVHKKMVVDV.....	
Q9XFJ4	FDEFKAAMQRDSSLQDVVLSSLRPN.....	
O35259	WYLPPMTREKDEDAVQFANRVKSAIARQEDW.....	
Q9FF57	WYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHS	

	551	568
SEQ ID NO: 8	.....	
P42322	.....	
Q9NKW7	.....	
Q9XFJ4	.....	
O35259	.....	
Q9FF57	ERKQQSFAESILARLEEK	

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Figure 19: Alignment of SEQ ID NO: 10 with Swiss Prot database

	1	50
Q24214	.....	
P28470	.....	
SEQ ID NO: 10	MTSTENTAMFTEDTSTLNGSTEANHAEFPLGERPTIGPEPPVNPFHESST	
O35259	.....METIMDDEVTKRTSAEEL	
Q9XFJ4	MGQREDIRTLSNEYEVTDIPRRGGLSVVRRGTRRRRTLHSGQHHEVVAIKT	
	51	100
Q24214	.....	
P28470	.....	
SEQ ID NO: 10	WSIPQVIKTILLVPLLVI RL LLSMFALMMLGYICVKVAMIGCKDPLFKPFN	
O35259	ESWNLLSRTNYNFYISRLRLTILWGLGV LIRYCFLLP.....	
Q9XFJ4	LRRFGPPPAPPEKKS LNKSRVPAAL ISETLLTNELLVMIKIVEDVSPHPN	
	101	150
Q24214	.....	
P28470	.....	
SEQ ID NO: 10	PLRRLLLVSVRLIARGVMVAMGYYYILVKGKPAHRSVAPIIVSNHIGFVD	
O35259	.....LRIALAF TGIGLLVVG.....TTMVG...	
Q9XFJ4	VIHLYDVCEDPSGVHLILELCSGGELFDRIAGQARYNEEGAAAVVRQIAK	
	151	200
Q24214	.....	
P28470	.....	
SEQ ID NO: 10	PIFVFYRHL PVI VSAKEIVEMPIIGMFLQALQIIPVDRINPASRHHAAGN	
O35259	.....YLPNGRFKEFLSKH....	
Q9XFJ4	GLEALHGASIVHRDLKPENCLFLNKDENSPLKIMDFGLSSIEDFANPVVG	
	201	250
Q24214	.....	
P28470	.....	
SEQ ID NO: 10	IRRRAMDNEWPHVMLFPEGTTTNGKALISFKTGAFSPGLPVQPMVIKYPH	
O35259	.....VHLMCYR.....	
Q9XFJ4	LFGSIDYVSPEALSREKITT KSDIWSLGVILYILLSGYPFFIAPSNRQKQ	
	251	300
Q24214	.....	
P28470	.....	
SEQ ID NO: 10	KYVNPCWCNQGGPLVILFQLMTQFVNYMEVEYLPVMTPNVHEIKNPHEFA	
O35259	.....ICVR.....ALTAITYHNRK	
Q9XFJ4	QMILNGQFSFDEK TWKNISSAKQLISSLLKVDPNMRPTAQEILEHPVWT	

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301 350  
Q24214 .....MGNETSLPME  
P28470 .....GNEASYHSE  
SEQ ID NO: 10 NRVRTAKALGVVCTEHN...LDIKLKMAAEKQPSGRSLVEFARME  
O35259 NRPR.....N.....GGICVANHT  
Q9XFJ4 GDLAKQEQMDAEIVSRLQSFNARRKFRAAAMASILSSSFSLRTKKLKKLV

351 400  
Q24214 MCSNFDADAEIRRLGKRFRKLDLD..NSGALSVDEFMSLPQLQ.QNPLVQR  
P28470 MGTHFDHDEIKRLGRSFKKMDLD..KSGSLSVDEFMSLPQLQ.QNPLVGR  
SEQ ID NO: 10 KLFRLDYSKAQEYLEKFSAMDPS..HSGYVTYDEFLKALHLP.PTQITEQ  
O35259 SRIDVIFASDGYAMVGQVHGG..LMGVIQRAMVKACPHVW.FERSEVK  
Q9XFJ4 GSYDLKPEELENLSHNFKKICKNGENSTLLEFEVLKAMEMSSLVPLAPR

401 450  
Q24214 VIDIFDADGNGEVDKFQFIQGVSQFS.VKGDKLSKLRFAFRIYDMDNDGY  
P28470 VIDIFDTDGNGEVDKFREFIVGTSQFS.VKGDDEQKLRFAFRIYDMDNDGF  
SEQ ID NO: 10 VFNLFDKNGHGSINFREFVAGLAFLS.THTSFQTTMKAAPKACDVGDT  
O35259 DRHLVAKRLTEHVQDKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVY  
Q9XFJ4 IFDLFDNNRDGTVDREIIGGFSSLK..YSQGDALRLCFQVYDTRSGC

451 500  
Q24214 ISNGELFQVLKMMVGNNLKD.TQLQQIVDKTIGFADKDEDGKISDFEFC  
P28470 ISNGELFQVLKMMVGNNLKD.WQLQQLVDKSILVLDKDGGRISFEFRD  
SEQ ID NO: 10 LTRNEVESSLMAVFP.....ELPPATVLKLFDTLDLNRDGSINWEEFSS  
O35259 PVAIKYDPQFGDAFWN.....SSKYGMVTYLLRMTSWAIVCS  
Q9XFJ4 ISKEEVESMLRALPEDCLPINITEPGKLDEIFDLMDANSKGKVTDFEKA

501 532  
Q24214 VVGNTDIHKKMVVDV.....  
P28470 VVRTMEIHKKLVVFDHGQED.....  
SEQ ID NO: 10 FLQRNPEYLAIILAAHPTLLQAPKSESEETNI  
O35259 VWYLPMTREKDEDAVQFANRVKSAIARQEDW  
Q9XFJ4 AMQRDSSLQDVVLSSLRPN.....

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Figure 20: Alignment of SEQ ID NO: 12 with Swiss Prot database

	1	50
Q9XFW4	.MAMAAVIVPLGILFFISGLVNNLLQAVCYVLRPMSKNTYRKINRVVA	
Q9SDN3	.....	
Q40119	MAIPAAAFIVPISLLFFMSGVLVNFQAVFYVLRPISKDTYRRINTLVA	
Q41745	MAIPLVLVVLPLGLLFLLSGLIVNAIQAVLFVTIRPFSKSFYRRINRFLA	
Q9SYC8	MKIPAALVFIPVGVLFLLISGLIVNIIQLVFFIIVRPFSRSLYRRINKNVA	
SEQ ID NO: 12	.....MIMM	
	51	100
Q9XFW4	ETLWLELVWIVDWWAGVKIQVFADDETFNRMGKEHALVVCNHRSDIDWL	
Q9SDN3	.....MGKEHALVISNHRSDIDWL	
Q40119	ELLWLELVWVIDWWAGVKVQLYTDTESFRLMGKEHALLICNHRSDIDWLI	
Q41745	ELLWLQLVWVVDWWAGVKVQLHADEETYSMGKEHALIISNHRSDIDWLI	
Q9SYC8	ELLWLQLIWLFDWWACIKINLYVDAETLELIGKEHALVLSNHRSDIDWLI	
SEQ ID NO: 12	EVLWSELIWLLDWWANVKVKVYTPKESWEHLGKEHALLICNHRSDIDWL	
	101	150
Q9XFW4	GWILAQRSGCLGSALAVMKKSSKFLPVIGWSMWFSEYLFERNWAKDEST	
Q9SDN3	GWVLAQRSGCLGSSLAVMKKSSKFLPVIGWSMWFSEYLFERSWAKDEGT	
Q40119	GWVLAQRSGCLSSSIAMKKSSKFLPVIGWSMWFSEYLFERNWAKDENT	
Q41745	GWILAQRSGCLGSTLAVMKKSSKFLPVIGWSMWFSEYLFERSWAKDEKT	
Q9SYC8	GWVMAQRVGCLGSSLAIMKKEAKYLPPIGWWSMWFSDYIFLERSWAKDENT	
SEQ ID NO: 12	GWIIAQRGLGCLGGTRAVMKKSTKFLPVIGWSMWFSEYVFLSRDWAKDEKV	
	151	200
Q9XFW4	LQSGLQRLNDFPRPFWLALFVEGTRFTTEAKLKAAQEYAASELVPVRNVL	
Q9SDN3	LKSGVQRLKDFPQPFWLALFVEGTRFTQAKLLAAQEYAAATGLPVVRNVL	
Q40119	LKSGLQRLNDFPKPFWLALFVEGTRFTKAKLLAAQEYAAAGLPVVRNVL	
Q41745	LKWGLQRLKDFPRPFWLALFVEGTRFTPAKLLAAQEYAAAGLPVVRNVL	
Q9SYC8	LKAGFKRLEDPMTFWLALFVEGTRFTQEKLEAAQEYASIRSLPSPVRNVL	
SEQ ID NO: 12	LKNGYSSLKGFPRTLWVLFVEGTRFTKAKLEVAQKFAADTGLRVPRVYL	
	201	250
Q9XFW4	IPRTKGFVSAVSNMRSFVPAIYDMTVAIPKTSPPPTMLRLFKGQPSVVHV	
Q9SDN3	IPRTKGFVTAVSQMRSFAPAIYDVTVAIPKSSPAPTMLRLFEGRPVVHV	
Q40119	IPRTKGFVSAVSNMRSFVPAIYDLTVAIPKTTEQPTMLRLFRGKSSVVHV	
Q41745	IPRTKGFVSAVSIMRDFVPAIYDTTVIVPKDSPQPTMLRILKGQSSVIHV	
Q9SYC8	IPRTKGFVSAVSEIRSFVPAIYDCTLTVHNNQPTPTLLRMFSGQSSEINL	
SEQ ID NO: 12	VPRTKGFVSAVENLREFVPVYDMTVAISKELPNPTMIRIFRGQPSVVHV	

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	251	300
Q9XFW4	HIKCHSMKDLPEPEDEIAQWCRDQFVAKDALLDKHIAADTFPGQKEQNIG	
Q9SDN3	HIKRHVMRDLPETDEAVAQWCKDIFVAKDALLDKHTVEQTFGDQQLKVTG	
Q40119	HLKRHLMKDLPKTDDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVQDIG	
Q41745	RMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTFD.EEIRPIG	
Q9SYC8	QMRRHKMSELPETDDGIAQWCQDLFITKDAQLEKYFTKDVFSDLVHQIN	
SEQ ID NO: 12	YVRRVPMSDLPEGANAISKWCHDAFHKDDRLEQHEKENTFGEDLYPIE	

	301	350
Q9XFW4	RPIKSLAVVSWACLLTLGAMKFLHWSNLFSSWKGIASAFGLGIITLCM	
Q9SDN3	RPLKSLLVVTAWACLLILGALKFLYWSSLLSSWKGIASFALGLGVTVLM	
Q40119	RPMKSLVVVSWMCLLCLGLVKFLQWSALLSSWKGMITTFVLGIVTVLM	
Q41745	RPVKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFTAAGMALVTGVM	
Q9SYC8	RPIKPLIVVIIWLGLVFGGFKLLQWLSIVASWKIILLFVFFLVIATITM	
SEQ ID NO: 12	RPLKPLIIVISWAITLLAAAWFLRR..VLSTWKGIAWVAGVLVVMLCV	

	351	391
Q9XFW4	QILIRSSQSERSTPAKVAPAKPKDNHQSGPSSQTEVEEKQK	
Q9SDN3	QILIRFSQSERSTPAPVAPTNNKNKGESSGKPEKQQ.....	
Q40119	HILIRSSQSEHSTPAKTRARQTAENPK.....	
Q41745	HVFIMFSQAERSSSARAARNRVKKE.....	
Q9SYC8	QILIQSSESQRSTPAKRPLQEQLISA.....	
SEQ ID NO: 12	QILVMSSQSERSSDPAKKANQKQAASVAHLGKTD.....	

Figure 21: **A.** Western blot analyses of the *Thraustochytrium* LPAAT expressed in *E. coli* as fusion protein (LPAAT-FP) with N-terminal GST tag and C-terminal His tag.

**B** Acyl-CoA specificity of the *Thraustochytrium* LPAAT expressed as GST fusion protein in *E. coli*

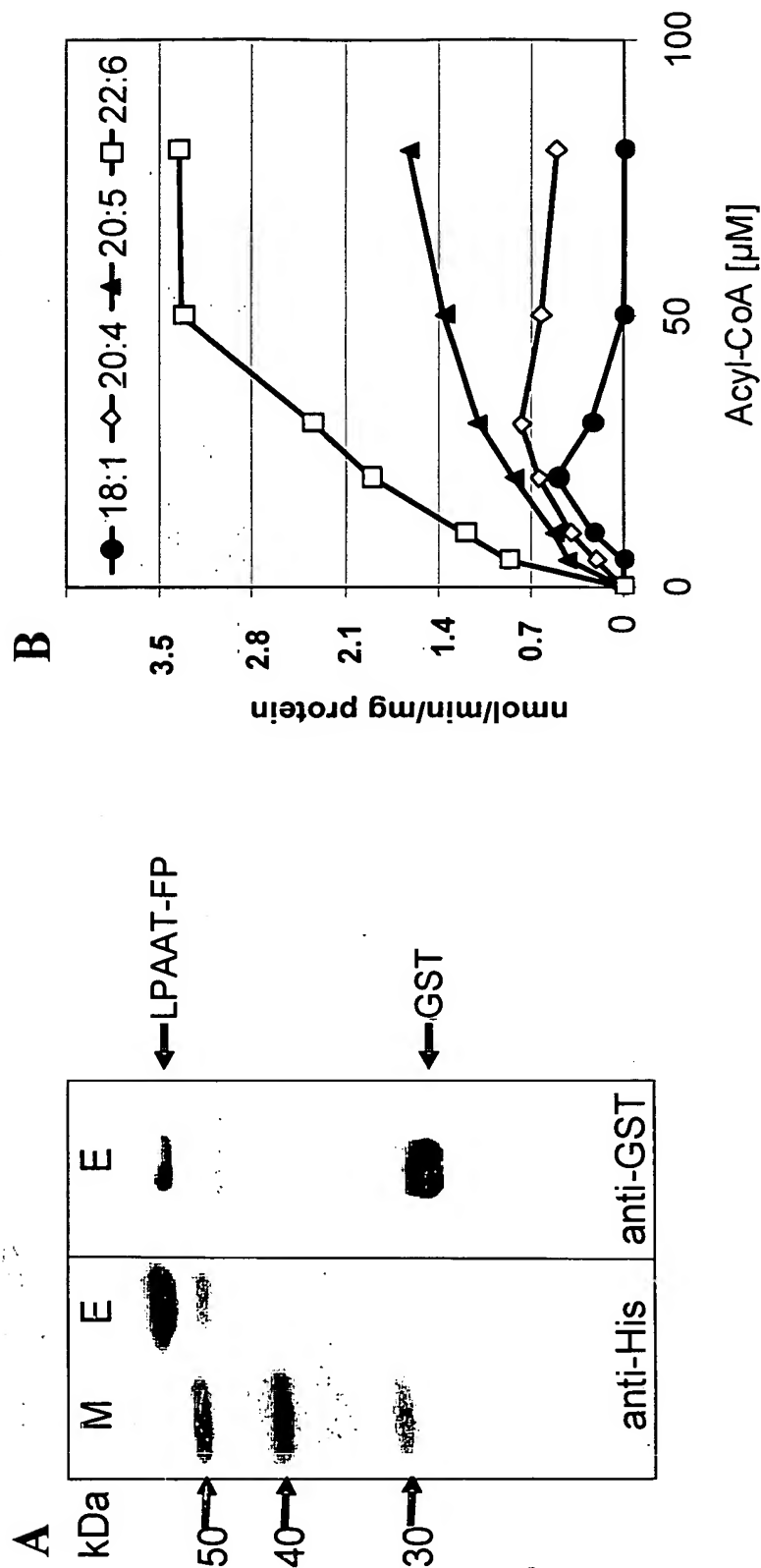
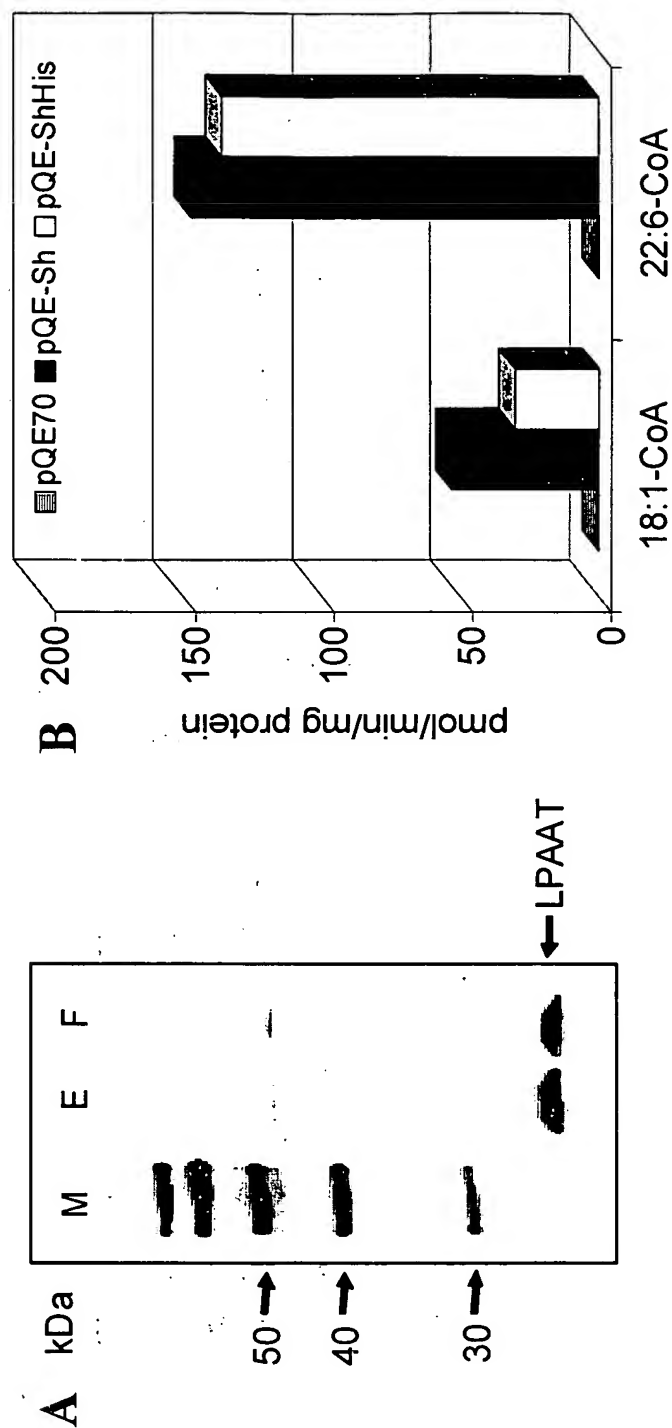
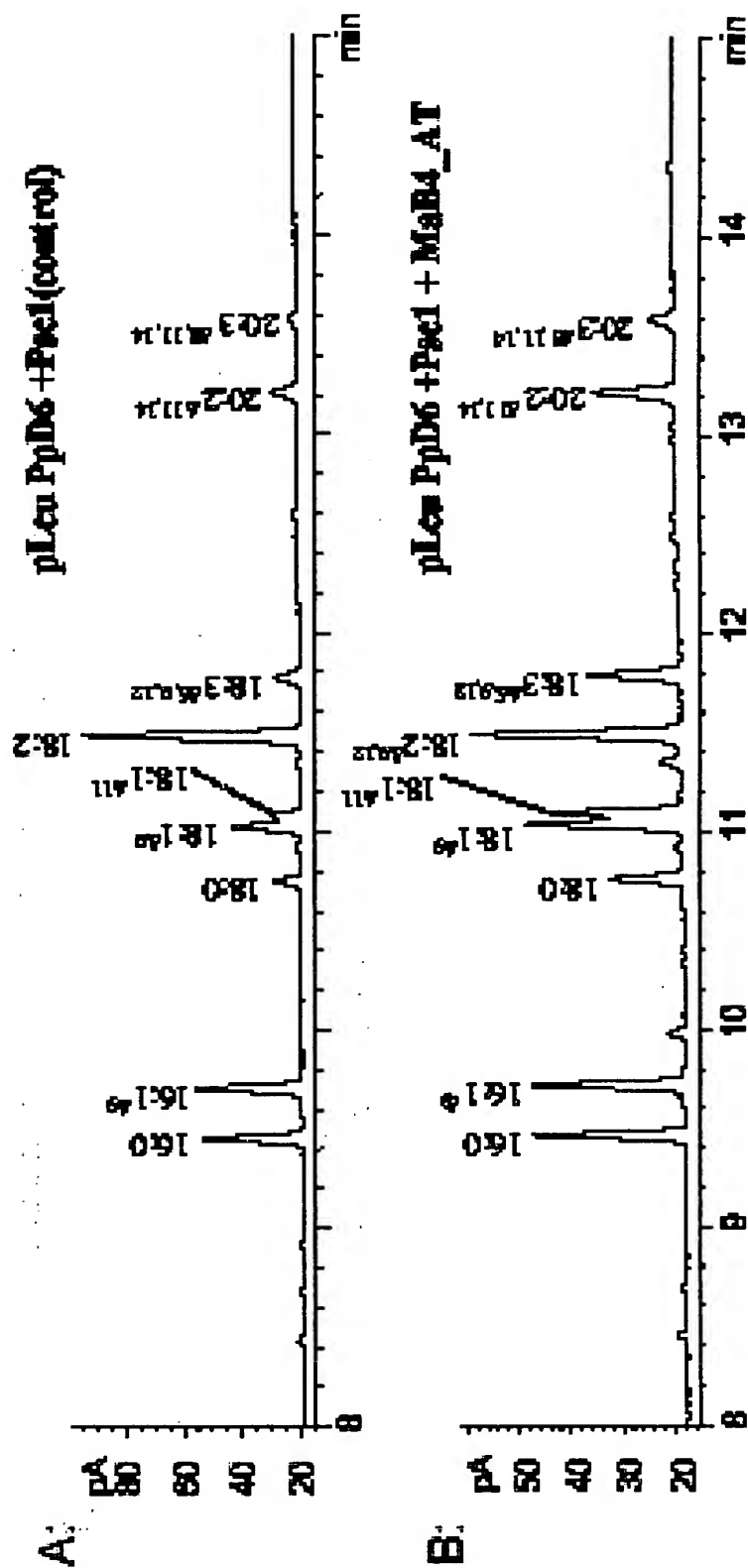




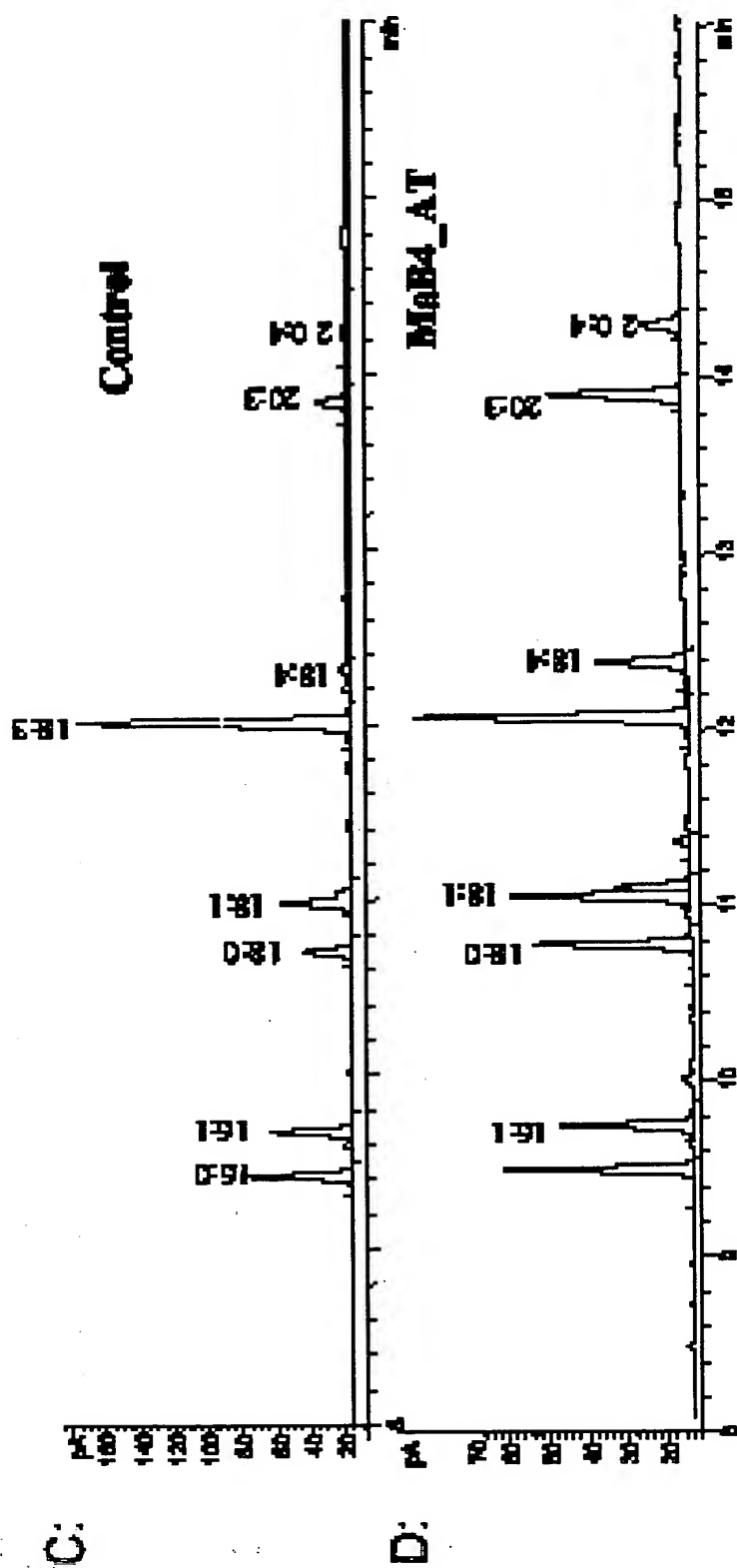
Figure 22: A: Western blot analysis of the *Shewanella* LPAAT expressed in *E. coli* as fusion protein with C-terminal His tag. B: Functional expression of the *Shewanella* LPAAT in *E. coli*



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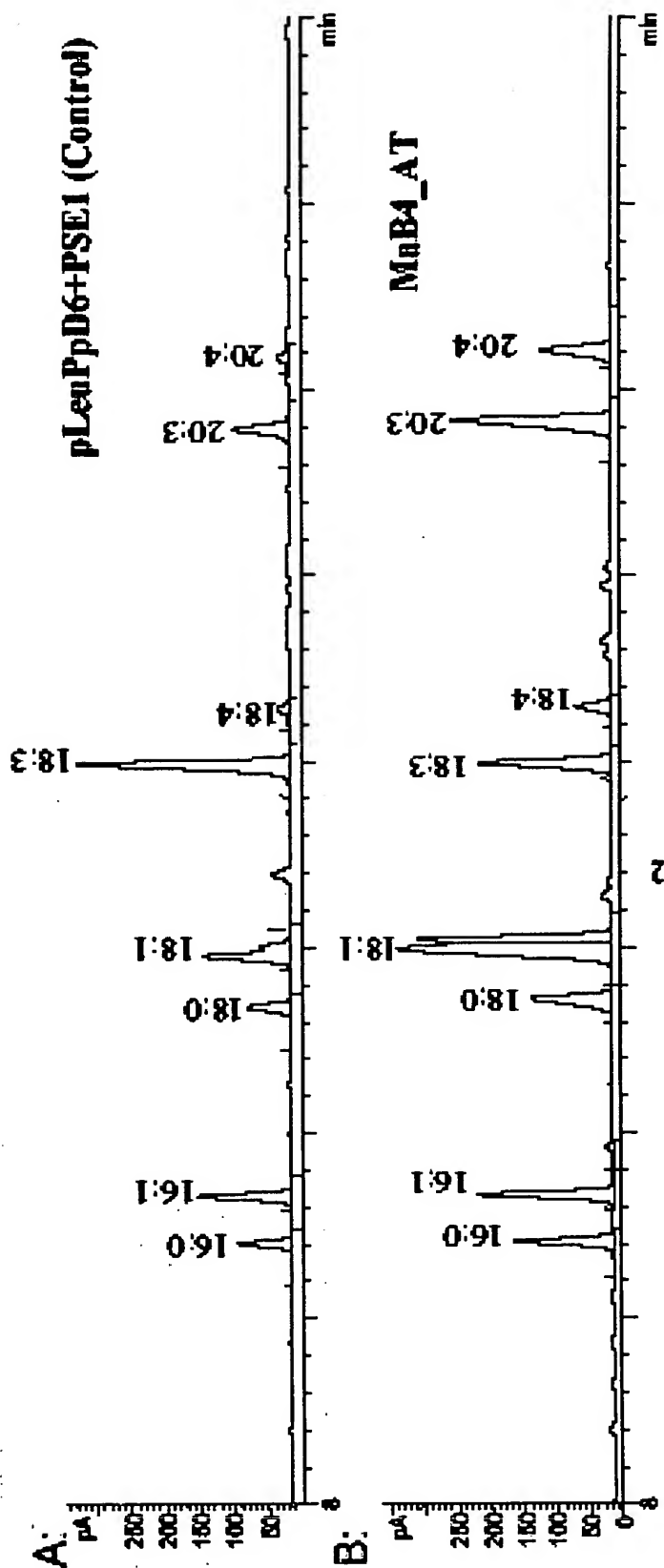
Figure 23: Expression of Mortierella LPAAT (MaB4\_AT) in yeast, and feeding of 18:2  $\Delta$ 9,12 fatty acids (A + B)

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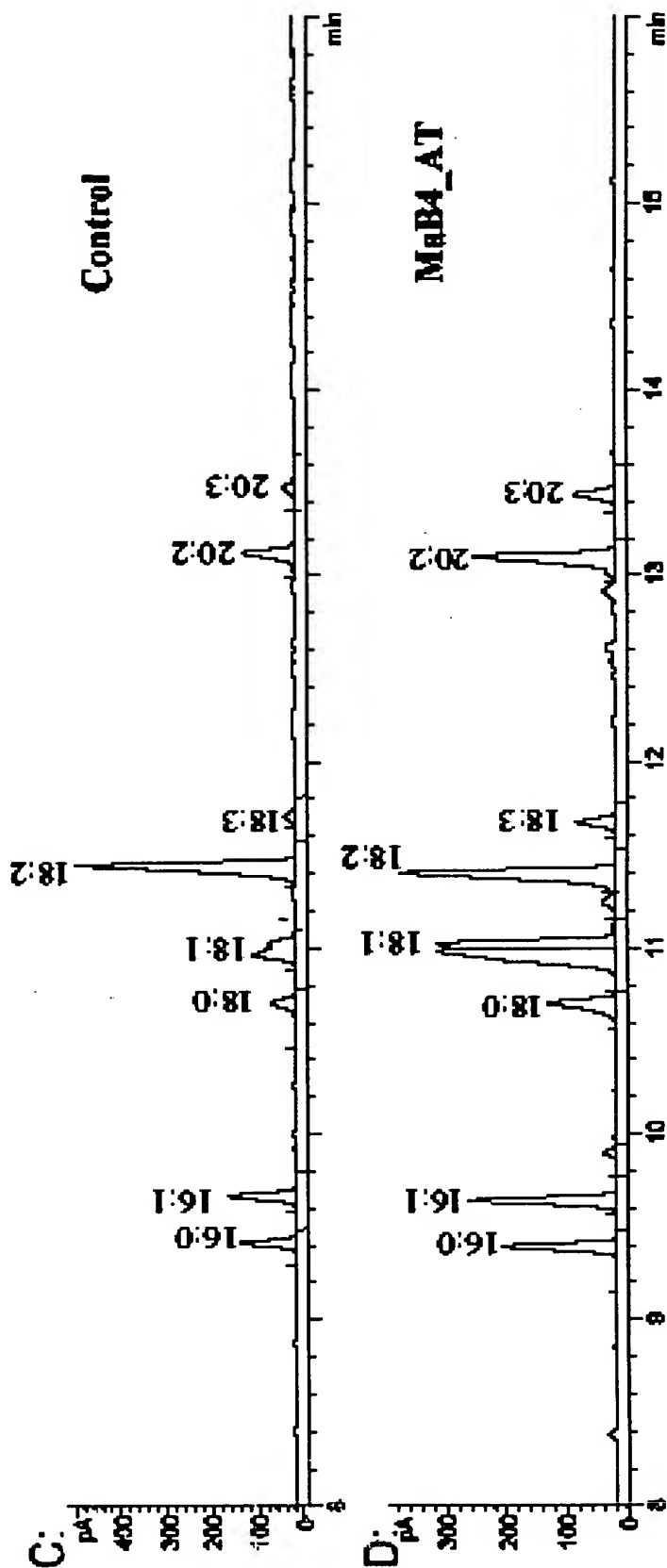
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Figure 25: Expression of Mortierella LPAAT (MaB4\_AT) in yeast, and feeding of 18:2  $\Delta$ 9,12 fatty acids (A + B). Analysis of the neutral lipids.



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Figure 26: Expression of Mortierella LPAAT (MaB4\_AT) in yeast, and feeding of 18:3  $\Delta$ 9,12,15 fatty acids (C + D). Analysis of the neutral lipids.



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